

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/29, 15/82, A01H 4/00		A1	(11) International Publication Number: WO 95/32288
			(43) International Publication Date: 30 November 1995 (30.11.95)
(21) International Application Number: PCT/US95/06505		(81) Designated States: CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
(22) International Filing Date: 22 May 1995 (22.05.95)		Published <i>With international search report.</i>	
(30) Priority Data: 08/248,474 25 May 1994 (25.05.94) US			
(71) Applicant: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA [US/US]; 22nd floor, 300 Lakeside Drive, Oakland, CA 94612-3550 (US).			
(72) Inventors: BIRD, David, McK.; 5676 Abilene, Riverside, CA 92506 (US). WILSON, Mark, A.; 29065 Gifford Avenue, Moreno Valley, CA 92555 (US).			
(74) Agent: BERLINER, Robert; Robbins, Berliner & Carson, 5th floor, 201 North Figueroa Street, Los Angeles, CA 90012-2628 (US).			
(54) Title: NEMATODE-INDUCED GENES IN TOMATO			
(57) Abstract			
<p>The present invention provides nucleic sequences from genes which are preferentially expressed in feeding site cells. These sequences can be used to produce transgenic plants resistant to nematode infection.</p>			
<p>ATTORNEY DOCKET NUMBER: 9341-028 SERIAL NUMBER: 09/978,274 REFERENCE: RE</p>			

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AT	Austria	GB	United Kingdom	MR	Mauritania
AU	Australia	GE	Georgia	MW	Malawi
BB	Barbados	GN	Guinea	NE	Niger
BE	Belgium	GR	Greece	NL	Netherlands
BF	Burkina Faso	HU	Hungary	NO	Norway
BG	Bulgaria	IE	Ireland	NZ	New Zealand
BJ	Benin	IT	Italy	PL	Poland
BR	Brazil	JP	Japan	PT	Portugal
BY	Belarus	KE	Kenya	RO	Romania
CA	Canada	KG	Kyrgyzstan	RU	Russian Federation
CF	Central African Republic	KP	Democratic People's Republic of Korea	SD	Sudan
CG	Congo	KR	Republic of Korea	SE	Sweden
CH	Switzerland	KZ	Kazakhstan	SI	Slovenia
CI	Côte d'Ivoire	LI	Liechtenstein	SK	Slovakia
CM	Cameroon	LK	Sri Lanka	SN	Senegal
CN	China	LU	Luxembourg	TD	Chad
CS	Czechoslovakia	LV	Latvia	TG	Togo
CZ	Czech Republic	MC	Monaco	TJ	Tajikistan
DE	Germany	MD	Republic of Moldova	TT	Trinidad and Tobago
DK	Denmark	MG	Madagascar	UA	Ukraine
ES	Spain	ML	Mali	US	United States of America
FI	Finland	MN	Mongolia	UZ	Uzbekistan
FR	France			VN	Viet Nam
GA	Gabon				

NEMATODE-INDUCED GENES IN TOMATO

BACKGROUND OF THE INVENTION

This invention was made with Government support
5 under Grant No. 89-37263-4355 awarded by the U.S.
Department of Agriculture. The Government has certain
rights in this invention.

The present invention relates to methods and nucleic
acid compositions for the production of transgenic plants
10 resistant to nematodes. In particular, it relates to
nematode-resistant transgenic plants comprising sequences
from nematode-induced genes.

Plant parasitic nematodes significantly affect the
productive capability of the world's farmlands. They
15 reduce the yield of the world's forty major food staples
and cash crops by an average of 12.3%, with losses
substantially higher for some commodities (e.g., 20.6%
for tomato). In the U.S. the reduced yields cause losses
of \$5.8 billion annually.

20 Especially significant in terms of crop losses are
the sedentary endo-parasites, cyst nematodes (*Globodera*
spp. and *Heterodera* spp.) and root-knot nematodes
(*Meloidogyne* spp.). Cyst nematodes generally infect
potatoes, soybeans, sugar beets, and wheat. Root-knot
25 nematodes affect over 2,000 species of plants, including
most of the major crops in the world.

Root-knot nematodes and cyst nematodes have similar
life-cycles. Infection occurs after larvae hatch in the
soil, invade the root and migrate intercellularly to the
30 developing vascular cylinder where permanent feeding
sites are established. Mature feeding sites are
characterized by the presence of multinucleate cells,
termed "giant cells" in root-knot nematode infections and
"syncytia" in cyst nematode infections. These large,
35 avacuolate cells with extensively remodeled cell walls
are metabolically active and serve as the obligate
nutritive source for the developing nematode. Giant cell

formation, coupled with limited proliferation of nearby pericycle and cortical cells results in the characteristic root-knot gall.

Today, nematode infections are controlled primarily
5 using chemical nematicides. These compounds are generally very toxic and have been suspected of causing environmental damage. These concerns have prompted efforts to find other methods of controlling nematodes in economically important crop plants. The present
10 invention addresses these and other needs.

SUMMARY OF THE INVENTION

The term "antisense orientation" refers to the orientation of nucleic acid sequence from a structural
15 gene that is inserted in an expression cassette in an inverted manner with respect to its naturally occurring orientation. When the sequence is double stranded, the strand that is the template strand in the naturally occurring orientation becomes the coding strand, and vice
20 versa.

The term "expression" refers to the transcription and translation of a structural gene so that a protein is synthesized.

A "feeding site cell" is an enlarged cell in a plant
25 root which is induced in response to nematode infection and provides nourishment to the developing nematode. Feeding site cells arising in response to root-knot nematode infections are termed giant cells, while those arising in response to cyst nematode infections are
30 termed syncytia.

A "nematode-induced" gene is one which is preferentially expressed in feeding site cells as compared to surrounding normal root tissue. The gene may be one which is normally expressed in other plant tissues
35 (e.g., leaf, cotyledon, apex, or hypocotyl) and is up-regulated in feeding site cells. Alternatively, the gene may be one that is not normally expressed in other plant

tissues, but is expressed only in response to nematode infection.

A "nematode-responsive" promoter is one which drives expression of an operably linked polynucleotide sequence only in, or substantially only in, feeding site cells. A promoter is considered to be nematode responsive if the level of expression of the operably linked polynucleotide sequence in cells other than feeding site cells is not sufficient to effectively disrupt cellular function. Thus, for example, if the sequence encodes a protein toxic to plant cells, plant cells other than feeding site cells are not adversely affected by the presence of a construct comprising the promoter and the structural gene.

"Nucleic acids" and "polynucleotides", as used herein, may be DNA or RNA. One of skill will recognize that the sequences from nematode-induced genes used in the methods of the invention need not be identical and may be substantially identical (as defined below) to sequences disclosed here. In particular, where a polynucleotide sequence is transcribed and translated to produce a functional polypeptide, one of skill will recognize that because of codon degeneracy a number of polynucleotide sequences will encode the same polypeptide. Similarly, because amino acid residues share properties with other residues, conservative substitutions of amino acids within a polypeptide may lead to distinct polypeptides with similar or identical function.

The term "operably linked" refers to functional linkage between a promoter and a second sequence, wherein the promoter sequence initiates transcription of RNA corresponding to the second sequence.

"Percentage of sequence identity" for polynucleotides and polypeptides is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the

polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Optimal alignment of sequences for comparison may be conducted by computerized implementations of known algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI, or BlastN and BlastX available from the National Center for Biotechnology Information), or by inspection. Sequences are typically compared using either BlastN or BlastX with default parameters.

Substantial identity of polynucleotide sequences means that a polynucleotide comprises a sequence that has at least 75% sequence identity, preferably at least 80%, more preferably at least 90% and most preferably at least 95%. Typically, two polypeptides are considered to be substantially identical if at least 40%, preferably at least 60%, more preferably at least 90%, and most preferably at least 95% are identical or conservative substitutions. Sequences are preferably compared to a reference sequence using GAP using default parameters.

Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine,

valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that polynucleotide sequences are substantially identical is if two molecules selectively hybridize to each other under stringent conditions. Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Typically stringent conditions for a Southern blot protocol involve washing at 65°C with 0.2XSSC.

The term "plant" includes whole plants, plant organs (e.g., leaves, stems, roots, etc.), seeds and plant cells. The class of plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including both monocotyledonous and dicotyledonous plants. It includes plants of a variety of ploidy levels, including polyploid, diploid and haploid.

A "polypeptide which inhibits nematode infection" is any polypeptide which when present in a cell infected by a nematode prevents formation of a feeding cell and/or

development of the nematode. Polypeptides which have this property can act by killing or disabling the infected cell or the nematode itself. Alternatively, the polypeptide may inhibit the activity of proteins and
5 other compounds necessary for feeding cell development. A number of polypeptides which inhibit nematode infection are described below.

The term "promoter" refers to a region of DNA upstream from the structural gene and involved in
10 recognition and binding RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells.

The phrase "selectively hybridizing to", refers to
15 a hybridization between a probe and a target sequence in which the probe binds substantially only to the target sequence when the target is in a heterogeneous mixture of polynucleotides and other compounds. Such hybridization is determinative of the presence of the target sequence.
20 Although the probe may bind other unrelated sequences, at least 90%, preferably 95% or more of the hybridization complexes formed are with the target sequence.

The phrase "substantially pure" or "isolated" when referring to a polynucleotide or protein, means a
25 chemical composition which is free of other subcellular components of the organism from which it is derived, e.g., tomato plants. Typically, a compound is substantially pure when at least about 85% or more of a sample exhibits a single polypeptide backbone, or
30 polynucleotide sequence. Minor variants or chemical modifications may typically share the same polypeptide sequence. Depending on the purification procedure, purities of 85%, and preferably over 95% pure are possible. Nucleic acid and protein purity or homogeneity
35 may be indicated by a number of means well known in the art, such as gel electrophoresis and the like.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a flow diagram outlining the strategy used to construct the cDNA library enriched for nematode-induced sequences.

5 Figure 2 shows the carboxyl terminus domain (CTD) of the deduced DB#117 gene product, aligned to show the heptamer repeat. The asterisk represents the carboxy terminus. In bold below is the canonical heptamer repeat for the CTD of the largest subunit of RNA polymerase II.

10 Figure 3 shows the deduced DB#280 gene sequence (bold) aligned with Myb sequences from Petunia, moss, the snapdragon 315 and 308 genes, barley, *Arabidopsis*, maize, *Drosophila*, and human. Database accession numbers are in brackets. Identical amino acids are indicated, +
15 represents conservative substitutions. None of the sequences have gaps.

Figure 4 shows alignment of the DB#226 sequence with the 3'UTR of the tobacco (*Nicotiana plumbaginiflora*) *pma-4* gene, which encodes a plasmalemma proton ATPase.

20

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The invention provides nucleic acid sequences from genes which are preferentially expressed in feeding site cells. These sequences can be used to produce transgenic
25 plants resistant to nematode infection.

Although feeding site cells, such as giant cells, share features with other plant cells, notably transfer cells, they are a novel cell type, and presumably arise by a pattern of gene expression different from that in
30 other plant cells. It has previously been speculated that gene expression in giant cells might include genes normally expressed at different developmental times or in different cell types (Bird, Mechanisms of the Meloidogyne-host interaction. In: *Nematology: from*
35 *molecule to ecosystem*. (1992) F. J. Gommers, and P. W. Th. Maas, eds. ESN Inc., Dundee, Scotland).

In a survey of randomly chosen, cloned root mRNAs, Evans et al. (*Mol. Gen. Genet.* 214:153-157 (1988)) were unable to identify any as being root-specific. Using a differential screen, Conkling et al. (*Plant Physiol.* 93:1203-1211 (1990)) isolated genes encoding four, moderately to abundantly expressed, root-specific transcripts from tobacco. The expression of one of these, TobRB7, has been reported to be up-regulated in giant cells induced in tobacco by *Meloidogyne incognita* (Opperman et al. 1994. *Science* 263:221-223). Also using a differential screening approach, Gurr et al. (*Mol. Gen. Genet.* 226:361-366 (1991)) identified a gene in potato whose expression is "correlated with events in the immediate vicinity of the pathogen" (potato cyst nematode, *Globodera rostochiensis*), but the nature of this gene was not revealed.

The present invention is based in part on the isolation of genes whose expression is up-regulated in giant cells as compared to normal root tissue. Although the methods described below relate to the analysis of nematode infected cells, the same approach can be used to identify genes induced by a variety of pathogens (e.g., bacteria, viruses, and fungi) in any crop plant of interest. One of skill will thus recognize that the recombinant DNA techniques for the control of nematodes described below, can also be applied to other pathogens in other crop plants.

Generally, the nomenclature and the laboratory procedures in recombinant DNA technology described below are those well known and commonly employed in the art. Standard techniques are used for cloning, DNA and RNA isolation, amplification and purification. Generally enzymatic reactions involving DNA ligase, DNA polymerase, restriction endonucleases and the like are performed according to the manufacturer's specifications. These techniques and various other techniques are generally performed according to Sambrook et al., *Molecular Cloning*

- A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989).

I. Isolation of nematode-induced genes and nematode-responsive promoters

5 The isolation of nematode-induced genes from plants may be accomplished by a number of techniques. Such genes are generally isolated using techniques designed to identify sequences specific to a particular tissue or cell types (see, e.g., Sambrook et al.) Such techniques
10 include differential hybridization techniques as described for instance in Gurr et al. *Mol. Gen. Genet.* 226:361-366 (1991). Briefly, in differential hybridization techniques a cDNA library prepared from feeding site cells is screened with probes generated from
15 cDNA derived from feeding site cells and normal root tissue. Those clones in the cDNA library which show increased hybridization to cDNA from feeding site cells are candidates for genes which are up-regulated in these cells. The clones identified in this way are then used
20 to screen a genomic library to isolate the corresponding gene.

 In addition, subtractive hybridization techniques can be used to prepare specific probes for screening cDNA or genomic libraries. These techniques can also be used
25 to prepare subtracted libraries enriched for the desired sequences. Subtractive screening or cDNA cloning approaches have proven effective in identifying transcripts with differential expression profiles. To ensure that cDNAs representing transcripts expressed in
30 low abundance are represented requires that enough cDNA remain after subtraction for efficient cloning. Methods have been developed using PCR and other techniques to ensure that low abundance transcripts are identified. A preferred subtractive hybridization technique using these
35 modifications is described in the Example section, below.

 Other techniques for the identification of nematode-induced genes can also be used. For instance,

oligonucleotide probes based on the sequences of previously identified nematode-induced genes can be used to isolate the desired gene in a cDNA or genomic DNA library. These techniques can be used to isolate
5 homologous genes in the same or different plant species. The use of such hybridization techniques for identifying homologous genes is well known in the art and need not be described further.

Alternatively, interposon tagging can be used
10 (Topping et al. 1991 *Developm.* 112:1009-1019 and Kertbundit et al. 1991 *Proc. Natl. Acad. Sci. USA* 88:5212-5216). In this method, a number of transgenic plants are produced each carrying a randomly integrated recombinant construct containing a promoterless reporter
15 gene, such as β -glucuronidase (GUS). Various tissues in the plant are then analyzed for expression of the reporter gene. If the reporter gene integrates in a site downstream from a promoter primarily active in a particular tissue, cells in the tissue will contain the
20 reporter gene product. Promoter sequences and genes that are primarily active in feeding site cells can thus be identified.

Once a desired genomic clone is identified, the 5' sequences can be analyzed to identify the promoter
25 sequence from the gene. This can be accomplished using deletion analysis and a promoterless reporter gene (e.g., GUS) to identify those regions which can drive expression of a structural gene.

Sequences characteristic of promoter sequences can
30 also be used to identify the promoter. Sequences controlling eukaryotic gene expression have been extensively studied. For instance, promoter sequence elements include the TATA box consensus sequence (TATAAT), which is usually 20 to 30 base pairs upstream
35 of the transcription start site. In most instances the TATA box is required for accurate transcription initiation. In plants, further upstream from the TATA

box, at positions -80 to -100, there is typically a promoter element with a series of adenines surrounding the trinucleotide G (or T) N G. J. Messing et al., in *Genetic Engineering in Plants*, pp. 221-227 (Kosage, Meredith and Hollaender, eds. 1983).

In addition, sequence comparison with promoters from other genes that are up-regulated in response to nematode infection can be used to identify regions of sequence homology among the genes. For example, comparison of the 5' flanking sequences of the sequences disclosed here can be used to identify common sequences. Alternatively, other genes previously identified as being nematode-induced (e.g., TobRB7) can be used.

Various methods relying on polymerase chain reaction (PCR) techniques to amplify the desired sequence can also be used. The amplified sequence is then subcloned into a vector where it is then sequenced using standard techniques. For example, PCR can be used to amplify a DNA sequence using a random 5' primer and a defined 3' primer. The 3' primer is based on the sequence of a cDNA isolated by differential screening or subtractive hybridization. The random 5' primer is then used to amplify genomic DNA upstream of the cDNA, to identify promoter sequences. Alternatively, genomic DNA can be cut at a suitable restriction site (determined from Southern blotting experiments) upstream from presumed promoter elements. A linker sequence is attached to the fragments and used as a specific 5' PCR priming site, along with the 3' primer based on the cDNA sequence.

Another approach is to use inverse PCR in which genomic DNA is restricted to generate a sticky ended molecule that spans known sequences at the 5' end of the gene and unknown promoter sequences. The DNA is ligated into circles and PCR amplified with a specific divergent primer pair designed from the cDNA sequence.

II. Production of nematode-resistant plants

Nematode-induced sequences, such as those described here, can be used in a variety of methods using recombinant DNA techniques for the control of nematodes in plants. For instance, the promoters from genes identified here can be used to drive expression of desired sequences in feeding site cells. The sequences can be structural genes encoding desired polypeptides or can be sequences which transcribe RNAs capable of inhibiting the expression of genes required for feeding site cell development. The promoters are used to ensure that the desired sequences are expressed only or substantially only in feeding site cells.

The polypeptides encoded by the structural genes will preferably prevent the development of the nematode in the plant in some way. For instance, the polypeptide may interfere with the transduction of the signal that leads to feeding cell formation in the host. Alternatively, polypeptides which have nematocidal or herbicidal activity can be used. The inhibitory RNAs may function in antisense suppression, sense suppression or as ribozymes.

A. Construction of expression vectors

The methods required for the recombinant expression of desired genes in transgenic plants are well known to those of skill in the art. Briefly, expression cassettes comprising a promoter from a nematode-induced gene operably linked to desired sequence such as a structural gene encoding a desired protein is introduced into the plant. Construction of appropriate expression vectors is carried out using standard techniques.

The minimal requirements of the vector are that the desired nucleic acid sequence be introduced in a relatively intact state. Thus, any vector which will produce a plant carrying the introduced DNA sequence should be sufficient. The selection of vectors and methods to construct them are commonly known to persons

of ordinary skill in the art and are described in general technical references (See, in general, *Methods in Enzymology* Vol. 153 ("Recombinant DNA Part D") 1987, Wu and Grossman Eds., Academic Press.

5 The recombinant vectors of the present invention typically comprise an expression cassette designed for initiating transcription of the desired polynucleotide sequences in plants. Companion sequences, of bacterial origin, are also included to allow the vector to be
10 cloned in a bacterial host. The vector will preferably contain a broad host range prokaryote origin of replication. A selectable marker should also be included to allow selection of bacterial cells bearing the desired construct. Suitable prokaryotic selectable markers
15 include resistance to antibiotics such as kanamycin or tetracycline.

Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art. For instance, in the case of *Agrobacterium*
20 transformations, T-DNA sequences will also be included for subsequent transfer to plant chromosomes.

For expression of polypeptides in plants, the recombinant expression cassette will contain, in addition to the desired polynucleotide sequence and the promoter
25 derived from a nematode-induced gene, a transcription initiation site (if the sequence to be transcribed lacks one), and a transcription termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette are typically included to allow for easy
30 insertion into a pre-existing vector.

The promoters can be modified as necessary to ensure that the desired polynucleotide sequence is expressed substantially only in response to nematode infection. A number of methods can be used to identify those sequences
35 within a given promoter that are responsible for a specific response to nematode infection. As noted above, sequences shared by promoters of nematode-induced genes

can be used to design promoters with the desired specificity. Alternatively, a reporter gene (e.g., GUS) can be operably linked to various deletion mutants of the promoter sequence and the ability of the modified
5 promoters to direct expression in feeding site cells and other tissues can be assayed (see, e.g., WO 93/06710).

In the construction of heterologous promoter/structural gene combinations, the promoter is preferably positioned about the same distance from the
10 heterologous transcription start site as it is from the transcription start site in its natural setting. As is known in the art, however, some variation in this distance can be accommodated without loss of promoter function.

15 As noted above, an expression cassette should also contain a transcription termination region downstream of the structural gene to provide for efficient termination. The termination region may be obtained from the same gene as the promoter sequence or may be obtained from
20 different genes.

If the mRNA encoded by the structural gene is to be efficiently translated, polyadenylation sequences are also commonly added to the vector construct. Alber and Kawasaki, *Mol. and Appl. Genet.*, 1:419-434, 1982.
25 Polyadenylation sequences include, but are not limited to the *Agrobacterium* octopine synthase signal (Gielen et al., *EMBO J.*, 3:835-846, 1984) or the nopaline synthase signal (Depicker et al., *Mol. and Appl. Genet.*, 1:561-573, 1982).

30 The vector will also typically contain a selectable marker gene by which transformed plant cells can be identified in culture. Usually, the marker gene will encode antibiotic resistance. These markers include resistance to G418, hygromycin, bleomycin, kanamycin, and
35 gentamicin. After transforming the plant cells, those cells having the vector will be identified by their

ability to grow in a medium containing the particular antibiotic.

Polypeptides which inhibit nematode infection

As noted above, the promoter can be used to drive
5 expression of structural genes encoding polypeptides
which inhibit nematode infection. A variety of
structural genes encoding protein or polypeptide products
which inhibit the infection by, for instance, inhibiting
the process of feeding cell development, promoting a
10 plant defense response, killing or disabling the plant
cell, or killing the nematode itself can be used. It is
preferred, particularly where the plant is a food plant,
that the polypeptide be non-toxic to animals, and
particularly be non-toxic to humans.

15 Polypeptides which inhibit feeding cell formation
will typically be competitive inhibitors of the nematode
signals which induce feeding cell formation. For
instance, proteins encoded by the sequences disclosed
here, which are shown to be involved in signal
20 transduction, can be used to design highly specific
inhibitors of feeding cell formation. In this embodiment
of the invention, the polypeptides preferably have
sequences substantially identical to those portions of
the signal transducing proteins which interact with the
25 appropriate ligand molecule. The signal transducing
proteins can also be used to design non-protein
inhibitors, which can be used as traditional nematicidal
agents.

Genes which produce antibodies immunoreactive with
30 molecules in the plant cell (e.g., proteins,
carbohydrates, and nucleic acids) can also be used to
inhibit the development of feeding cells (see, e.g., Huse
et al., *Science* 246, 1275-1281 (1989)). As used here the
term "antibody" refers to a variety of forms of
35 immunoglobulin molecules besides whole antibodies,
including for example, Fv, Fab, and F(ab)₂ fragments,
single chains and the like. Plant proteins to which such

antibodies can be directed include, but are not limited to, RNA polymerase, respiratory enzymes, cytochrome oxidase, Krebs cycle enzymes, protein kinases, aminocyclopropane-1-carboxylic acid synthase, and enzymes
5 involved in the shikimic acid pathway such as enolpyruvyl shikimic acid-5-phosphate synthase. Nematode proteins or nematode-induced molecules 'can' also be targeted. Examples include low molecular weight compounds, with few or no features in common with normal plant products, such
10 as hormones or elements of the signal transduction pathway. Products that play a role in signaling between plants and other organisms (e.g., the nod factor) can also be targeted. Preferred antigens include compounds secreted through the nematode's feeding stylet that
15 initiate and/or maintain feeding cells.

Another class of structural genes which can be used in the invention are those induced by plant pathogens (e.g., nematodes, bacteria, fungi and the like) and that elicit a hypersensitive or other defense responses in
20 plants. Thus, a gene which is normally responsive to a particular pathogen (or to nematodes in another plant species) is made responsive to nematode infection in the transgenic plant. An example of a suitable nematode-inducible gene is the Mi gene from tomato. Examples of
25 suitable genes responsive to other pathogens are reviewed in Stintz et al. *Biochemie* 75:687-706 (1993).

Phytotoxic polypeptides used in the invention may either kill the plant cell in which they are expressed or simply disable the cell so that it is less capable of
30 supporting the pathogen. Examples of suitable structural genes encoding phytotoxic polypeptides include genes encoding enzymes capable of degrading nucleic acids (e.g., nucleases, restriction endonucleases micrococcal nuclease, and ribonucleases such as Rnase A and barnase)
35 and enzymes which attack proteins (e.g., trypsin, pronase A, carboxypeptidase, endoproteinase Asp-N, endoproteinase Glu-C, and endoproteinase Lys-C). Other examples include

toxins from plant pathogens (e.g., phaseolotoxin, tabtoxin, and syringotoxin), lipases from porcine pancrease and *Candida cyclindracea*, as well as membrane channel proteins such as glp F and connexins.

5 Structural genes which are specifically target nematodes include those encoding *Bacillus thuringiensis* toxins as described, for instance, in EP 517, 367 A1. Other proteins include proteinase inhibitors such as cowpea trypsin inhibitor as described in WO 92/15690 or
10 proteins which affect nematode sensory behavior such as miraculin.

Sequences which inhibit expression of nematode-induced genes

Recombinant techniques can also be used to inhibit
15 expression of particular genes which are required for development of feeding site cells. In these techniques inhibitory RNAs (i.e., those which inhibit the expression of target genes) are transcribed in feeding site cells. Promoters from nematode-induced genes are preferably used
20 to direct transcription of the inhibitory RNA sequences only in feeding site cells and thus prevent development of the pathogen. If the target gene is expressed only in feeding site cells, other constitutive or inducible promoters well known to those of skill in the art can
25 also be used. For instance, the 35S promoter from cauliflower mosaic virus may be used. Alternatively, inducible promoters which direct expression only in root tissue can be used.

In some embodiments, antisense regulation of the
30 gene can be used. To accomplish this, a polynucleotide sequence from the desired gene is cloned and operably linked to a promoter (e.g., a promoter from a nematode-induced gene) such that the anti-sense strand of RNA will be transcribed. The construct is then transformed into
35 plants and the anti-sense strand of RNA is produced. In plant cells, it has been shown that anti-sense RNA inhibits gene expression by preventing the accumulation

of mRNA which encodes the enzyme of interest, see, e.g., Sheehy et al., *Proc. Nat. Acad. Sci. USA*, 85:8805-8809 (1988), and Hiatt et al., U.S. Patent No. 4,801,340.

In other embodiments, cloned polynucleotide
5 sequences configured such that the sense-strand of RNA is produced can be used to block the transcription of target genes in plants. For an example of the use of this method to modulate expression of endogenous genes see, Napoli et al., *The Plant Cell* 2:279-289 (1990), and U.S.
10 Patent No. 5,034,323.

A third approach is the use of catalytic RNA molecules or ribozymes. Ribozymes can be designed to specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific
15 location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs
20 confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified in the literature. One class of ribozymes is derived from a number of small circular RNAs which are
25 capable of self-cleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus,
30 velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. Analysis of the self-cleaving RNAs reveals the presence of a conserved regions necessary for cleavage and allows the design of ribozymes specific for a target RNA. The
35 design and use of target RNA-specific ribozymes is described in Haseloff et al. *Nature*, 334:585-591 (1988).

The inhibitory nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the target nematode-induced gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors for use in the present invention can be designed such that the inhibitory effect applies to one or more genes within a family of genes exhibiting homology or substantial homology to the target gene. Similarly, segments from nematode-induced genes from tomato can be used to inhibit expression of homologous genes in different plant species, e.g., using sense or antisense suppression techniques described herein either directly or as a means to obtain the corresponding sequences to be used to suppress the gene.

The introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA. Generally, higher homology can be used to compensate for the use of a shorter sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments will be equally effective. Normally, a sequence of between about 30 or 40 nucleotides and about 2000 nucleotides should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of at least about 500 nucleotides is especially preferred.

B. Plant Transformation

The various DNA constructs described above may be introduced into the genome of the desired plant by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using polyethylene glycol precipitation (Paszkowski et al. *Embo J.* 3:2717-2722 (1984)) electroporation and microinjection of plant cell protoplasts (Fromm et al. *Proc. Natl. Acad. Sci. USA*

82:5824 (1985)), or the DNA constructs can be introduced into plant tissue using ballistic methods, such as DNA particle bombardment (Klein et al. *Nature* 327:70-73 (1987)). Alternatively, the DNA constructs may be
5 combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell
10 DNA when the cell is infected by the bacteria. For a review of gene transfer methods for plant and cell cultures see, Potrykus *CIBA Found. Symp.* 154:198 (1990).

Agrobacterium tumefaciens-mediated transformation techniques are the most commonly used techniques for
15 transferring genes into plants. These techniques are well described in the scientific literature. See, for example Horsch et al. *Science* 233:496-498 (1984), Fraley et al. *Proc. Natl. Acad. Sci. USA* 80:4803 (1983), and Hooykaas *Plant Mol. Biol.* 13:327-336 (1989).

20 All species which are a natural plant host for *Agrobacterium* are transformable *in vitro*. Most dicotyledonous species can be transformed by *Agrobacterium*. Monocotyledonous plants, and in particular, cereals, are not natural hosts to
25 *Agrobacterium*. There is growing evidence now that certain monocots can be transformed by *Agrobacterium*. Using novel experimental approaches cereal species such as rye (de la Pena et al., *Nature* 325:274-276, 1987), corn (Rhodes et al., *Science* 240:204-207, 1988), and rice
30 (Shimamoto et al., *Nature* 338:274-276, 1989) may now be transformed.

After transformation, transformed plant cells or plants comprising the introduced DNA must be identified. A selectable marker, such as those discussed above is
35 typically used. Transformed plant cells can be selected by growing the cells on growth medium containing the

appropriate antibiotic. The presence of opines can also be used if the plants are transformed with *Agrobacterium*.

After selecting the transformed cells, one can confirm expression of the desired transgenic structural
5 gene or inhibitory RNA. Simple detection of mRNA encoded by the inserted DNA can be achieved by well known methods in the art, such as Northern blot hybridization. The inserted sequence can be identified using the polymerase chain reaction (PCR) and Southern blot hybridization, as
10 well. See, e.g., Sambrook, *supra*.

Transformed plant cells (e.g., protoplasts) which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired
15 nematode resistant phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell*
20 *Culture*, pp. 124-176, MacMillilan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration
25 techniques are described generally in Klee et al. *Ann. Rev. of Plant Phys.* 38:467-486 (1987).

One of skill will recognize that after the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced
30 into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

The invention has use in producing nematode resistant cultivars of any plant susceptible to infection
35 by these pathogens. The invention thus has use over a broad range of plants, including species from the genera *Trifolium*, *Medicago*, *Phaseolus*, *Pisum*, *Vigna*, *Glycine*,

Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Capsicum, Datura, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Cichorium, Helianthus, Chrysanthemum, Vitus, Lactuca, 5 Asparagus, Cucumis, Cucurbita, Malus, Pyrus, Prunus, Rosa, Fragaria, Tarro, Ananas, Musa, Cacao, Beta, Coffea, Gossypium, Thea, Dioscorea, Arachis, Citrullus, Juglans, Olea, Cannabis, Triticum, Hordeum, Avena, Festuca, Sorghum, Oryza, Secale, and Zea.

10 The following examples illustrate, but do not limit, the invention:

Example 1

This example describes the construction of a cDNA bank representing genes either uniquely expressed in 15 giant cells (compared to uninfected root cells) or with elevated expression levels. The methods used here combine PCR amplification of cDNA with the efficient and sensitive phagemid subtraction methods to produce a subtracted cDNA bank from a small number of individual 20 tomato giant cells (see, Bird and van der Knaap *Phytopathology* 84:299-303 (1994)). A flow chart outlining the strategy used to construct the library is shown in Figure 1.

MATERIALS AND METHODS

25 Culture maintenance. Giant cells and normal root tissue were isolated from *in vitro* cultured tomato (*Lycopersicon esculentum* cv 'Rutgers Large Red') plants. Seeds were surface sterilized by vacuum infusion of 0.5% sodium hypochlorite and germinated in parafilm-sealed, 30 petri plates on 2% GelRite containing vitamin supplemented Gamborg's B5 medium. Cultures were maintained in the dark at 26 °C. When tertiary root branches were evident (approximately 2 weeks), each dish was inoculated with 200 root-knot nematode (*Meloidogyne* 35 *incognita*) eggs, surface sterilized by incubation for 10 min in 0.1% streptomycin, 0.0 1% HgCl₂. Nematode stocks were maintained on greenhouse grown tomato (cv 'Tropic')

plants, and eggs isolated by hypochlorite extraction (McClure et al. *J. Nematol.* 5:230 (1973)).

Root galls containing young adult female nematodes were excised from the etiolated plant-nematode cultures at 1 to 2 months post infection. Gall tissue surrounding the giant cell was dissected away and the exposed, intact nematode removed. Giant cells were resected and snap frozen at -72 °C.

RNA isolation. RNA was isolated by a modification of the method of Chomczynski and Sacchi *Anal. Biochem.* 162:156-159 (1987). Approximately 50 mg of giant cells were ground under liquid nitrogen in a micro-homogenizer (Biomedix, Middlesex, UK) and resuspended in 200 µl E-buffer (4M guanidinium isothiocyanate, 25mM sodium phosphate buffer, pH 7.4, 1% sarkosyl, 1 mM β-mercaptoethanol) at 40° C. The suspension was incubated at 40° C, 20 min, with occasional vortexing. Sodium acetate pH 4 was added to 50 mM followed by an equal volume of water saturated phenol, and the sample placed on ice for 10 min. One-tenth volume of chloroform was added and the aqueous phase recovered following centrifugation at 12,000g for 10 min at 4° C. The organic phase was back-extracted with 100 µl E-buffer containing 50 mM Na-acetate pH 4 and the aqueous phases pooled. RNA was recovered by ethanol precipitation, dried in vacuo and dissolved in water.

Normal root RNA was extracted from uninfected tissue cultured seedlings grown in parallel and harvested at the same times as giant cells. Freshly harvested tissue was frozen in liquid nitrogen and ground in a mortar and pestle. E-buffer was added at two ml per gram fresh weight of tissue.

cDNA synthesis. Poly-A (+) RNA was captured from giant cell total RNA on oligo-dT₂₅ coupled paramagnetic beads (DynaI Inc., Great Neck, N.Y.) according to the manufacturers instructions. Bead-bound RNA was washed twice with 2.5 times the original bead suspension volume

of first strand cDNA synthesis buffer (50 mM Tris HCl pH 8.0, 50 mM KCl, 10 mM MgCl₂) and cDNA was synthesized on the bead to produce a solid phase primary cDNA pool. First and second strand synthesis and end repair reactions were performed using the Riboclone cDNA synthesis system (Promega, Madison, WI) according to manufacturers suggestions. Beads were kept in suspension during the synthesis reactions by shaking at 350 rpm.

Oligonucleotides P35 (GTAAGCGGCCGCGTCAGTAACTC, Seq. I.D. No.:110) and P36 (TACTGACGCTGCGGCCGCTTAC, Seq. I.D. No.:111) were annealed using standard conditions (Wu et al. *Meth. Enzymol.* 152:343-349 (1987)). This formed a double stranded adapter molecule, blunt at one end and with a non-complementary, four-base overhang at the opposite end, with an internal NotI site. P36 was end-labeled prior to annealing using polynucleotide kinase. Annealed adapter was ligated onto the free end of the bead-bound dscDNA at 15° C for 16 h with shaking at 350 rpm. Unligated adapter was removed from the cDNA by washing with sterile water until free counts were no longer detected in the wash.

Second strand cDNA was eluted from bead-bound first strand by heating to 94° C for three minutes. The beads were then snap chilled on ice and the aqueous phase removed from the beads. cDNA yield was estimated by liquid scintillation counting of an aliquot of the eluate. An additional batch of second strand cDNA was synthesized on the beads by primer extension with P36. Following elution, this material was pooled with the previously synthesized second strand cDNA. Pooled cDNA was converted to double stranded form by extension from the poly-A tract at the 3'-end with P39 primer [ACTCTTGGGCCGAGTTGGCC(T)₁₅] (Seq. I.D. No.:112). The dscDNA was purified from excess P39 by spin column chromatography over Sephadex G-50 equilibrated with 200 mM NaCl.

PCR amplification. One fourth of the cDNA was amplified by 15 cycles of PCR (94° C, 2 min; 58° C, 1 min; 72° C, 5 min) using primers P40 [ACTCTTGGGCCGAGTTGGCC(T)₄] (Seq. I.D. No.:113) and P36.

- 5 Amplification products were fractionated on 1% LMP agarose and size ranges of DNA (400 - 700 bp, 700 bp - 1.3 kb, 1.3 kb - 5 kb) resected and eluted by Gelase digestion (Epicentre Technologies, Madison, WI). One-fifth of each size class was re-amplified by 10 cycles of
- 10 PCR, using the same conditions as the original amplification. Each reaction was diluted five fold onto fresh reaction mix, and amplified a further 5 cycles. The 400 - 700 bp, 700 bp 1.3 kb fractions faithfully re-amplified, and were pooled.

- 15 cDNA cloning. Single stranded amplification products were removed by mung bean nuclease digestion, and the cDNA was cut with *NotI* and *SfiI*. Fifty ng of restricted cDNA insert was ligated into 300 ng of dephosphorylated, *NotI-SfiI* digested pGem 11zf(+) vector
- 20 (Promega, Madison, WI). The ligation reaction was phenol extracted, ethanol precipitated, resuspended in 4 μ l water, and electroporated at 200 Ω , 25 μ F, 18.8 kV/cm into 200 μ l of electrocompetent *E. coli* DH12s cells (BRL, Gaithersburg, MD). Cells were incubated for 40 minutes
- 25 in 100 ml SOC medium at 37° C with shaking (350 rpm) and an aliquot was removed to determine the number of primary transformants. Ampicillin was added to 50 μ g per ml and the culture grown to an A₆₀₀ of 0.1. Two milliliters were removed, grown overnight at 37° C and stored as a
- 30 glycerol stock. M13K07 phage were added to the main culture at an moi of 10, and the culture grown for a further 2 h. Phage infected cells were selected by addition of kanamycin to 70 μ g/ml, and the culture incubated with vigorous shaking at 37° C for 15 h.

- 35 Recombinant M13 virions were harvested by polyethylene glycol precipitation, and ssDNA prepared and resuspended in 200 μ l water. The sample was digested

with *Hind*III and ssDNA purified by fractionation on LMP agarose.

Driver preparation. A solid phase cDNA pool was prepared from 75 μ g of uninfected-root total RNA and 10 ng of the resultant double stranded cDNA subjected to 15 cycles of PCR, exactly as described for the giant cell library, except the dTTP concentration was reduced to 75 μ M and biotin-16-dUTP (Boehringer Mannheim, Indianapolis, IN) added to 25 μ M (Lebeau et al. *Nuc. Acids Res.* 19:4778 (1991)). The reaction was diluted five fold and PCR amplification continued for 5 cycles. The final yield of biotinylated cDNA was ~5 μ g.

Subtraction and transformation. Biotinylated root cDNA (4 μ g) was coprecipitated with 2 μ g M13 DNA with giant cell cDNA inserts, giving a ten fold molar excess of driver to insert. The DNA was resuspended in 20 μ l water, and 0.5 μ g oligo-dT₁₈ added. One microliter of 2 X hybridization solution (400mM NaCl, 100 mM Tris HCl pH 7.5, 4 mM EDTA) was added, and the mixture dried in vacuo to 2 μ l. The solution was covered with a drop of mineral oil, heated to 94° C 5 min, and incubated 65° C for 25 h.

The annealing reaction was diluted to 50 μ l with 0.5 X SSC and then incubated at room temp for 30 min with 600 μ l streptavidin coated paramagnetic beads (Promega, Madison WI), previously equilibrated to 0.5 X SSC. Beads were separated from the solution on a magnetic stand, and the binding step repeated. Oligo dT₁₈ was removed from unbound ssDNA by fractionation on Sephadex G-50/200 mM and salts removed by fractionation on water equilibrated Sephadex G-50. ssDNA was transformed to double stranded form by Klenow extension from P46 primer [GGCCAAGTTGGCC(T)₅] (Seq. I.D. No.:114), de-salted on water saturated Sephadex G-50, dried to 3 μ l in vacuo and electroporated into *E. coli* DH12s cells. Cells were recovered for one hour in SOC medium and plated with an X-gal/IPTG screen. Insert containing colonies were

picked into individual wells of 96 place microtiter plates and glycerol stocks prepared.

Library analysis. Glycerol stocks were replica-stamped onto nitrocellulose membranes and were probed
5 with nick-translated genomic tomato and nematode DNA and cDNA inserts using standard conditions (Wahl et al. *Proc. Natl. Acad. Sci. USA* 76:3683-3687' (1979)).

ssDNA was prepared from recombinants by rescue with the helper phage M13K07 and subjected to sequencing using
10 the dideoxy chain-termination method (Sanger et al., *Proc. Natl. Acad. Sci. USA* 74:5463 (1977)). Hybridization probes for Southern and RNA dot blot analyses were prepared by primer extension of single stranded templates with universal sequencing primer.
15 Tomato and nematode genomic DNA was prepared by grinding in liquid nitrogen followed by proteinase K digestion and phenol/chloroform extraction.

RESULTS

cDNA synthesis. Fifty one milligrams of essentially
20 pure giant cells were accumulated by dissection. Based on comparative ethidium bromide fluorescence, the yield of total RNA from this sample was estimated to be 11 μ g. This represents a yield per gram fresh weight of tissue of approximately 4 fold higher than we obtain from
25 cultured whole roots, and possibly is a reflection of increased transcriptional activity in giant cells.

Performing the cDNA synthesis on paramagnetic beads provided a number of advantages over liquid synthesis, including the ability to readily recover poly-A(+) RNA
30 and cDNA into essentially zero volume. Because the bead effectively blocked one end, addition of a *NotI* adapter after cDNA synthesis was restricted to the 5'-end (with respect to the message). Additionally, the use of solid phase cDNA synthesis provided a reusable pool of first
35 strand cDNA.

Based on incorporation of 32 P-labeled P36 (half of the adapter), conversion of poly-A(+) RNA into eluted

second strand cDNA was 24%. Subsequent re-synthesis of second strand cDNA corresponded to a 15% conversion of poly-A(+) RNA. It is likely that this reduced efficiency resulted from inefficient priming. Conversion of pooled,
5 eluted second strand cDNA to double stranded form by priming with an oligo-dT-anchored, *Sfi*I primer (P39) yielded 43 ng of double stranded cDNA. Analysis of an aliquot by electrophoresis on alkaline agarose revealed an average size of 800 bases for this cDNA pool, with a
10 portion extending larger.

Pilot experiments indicated that, under our conditions, the rate of amplification began to diminish between 10 and 15 rounds of PCR while, in pari passu, the amount of single stranded product increased.
15 Consequently, the giant cell cDNA was subjected to only 15 cycles of PCR amplification prior to size fractionation. The size classes were re-amplified and single stranded strand amplification products removed by mung bean nuclease digestion prior to cloning.
20 Comparison of cDNA before and after nuclease treatment indicated that up to two thirds of the amplified cDNA, primarily the larger material, consisted of single strand product. The average size of the final cDNA population was about 300 bp, with a range of 200 to 500 bp.
25 Preferential extension of smaller cDNAs over larger ones as PCR progresses has been observed previously (Belyavsky et al. *Nuc. Acids Res.* 17:2919-2932 (1989)).

Cloning. To maximize the efficiency of the cloning step, and also to eliminate the possibility of cloning
30 uninfected-root driver cDNA, amplified giant cell cDNA was ligated into a phagemid vector. A test plating of the library at this stage indicated that it contained 1.4×10^6 transformants. Following conversion to single stranded form by rescue with M13K07, the cloned giant
35 cell cDNAs were annealed with normal-root cDNA driver to a Cot value of 500. Using a k value for a typical mammalian cell (15,000 unique transcripts), the fraction

of cDNAs common both to uninfected roots and giant cells that have annealed at Cot 500 is 96.5%.

After the annealed cDNA had been removed, the single stranded recombinants were converted to double stranded
5 form. Transformation by electroporation of double stranded plasmid DNA has been shown to be several hundred fold more efficient than single stranded plasmid DNA. We utilized a primer which spans the *Sfi*I cloning site and the poly-A tail of the insert. This primer is not
10 complementary to either insert-minus or to incorrectly oriented insert-containing clones. Production of double stranded plasmid DNA prior to transformation with this primer allowed for more efficient cloning of genuine subtracted clones over insert-minus or aberrant clones
15 which may have escaped the subtraction procedure. *

Following transformation, 287 insert-containing clones, as determined by blue/white colony screening, were recovered. This corresponded to an overall enrichment of 4,860 fold of giant cell sequences over
20 normal root sequences present in the cDNA library. This figure is substantially higher than is typically obtained by subtraction.

Library analysis. A variety of criteria were used to assess the overall quality of the subtracted library.
25 Insert size was determined by restriction analysis. Inserts resected from ten randomly selected clones ranged in size from 200 to 500 bp in length. Seven of these probes were also hybridized back to the entire library. One clone detected two recombinants; the remaining six
30 probes detected only the clones from which they were constructed. This result suggests that the complexity of the subtracted library might be high.

The total number of highly repeated genomic sequences represented in the library was determined by
35 hybridization of replica filters with nick translated tomato total genomic DNA. Forty two of the 287 clones gave a high signal. Four of these clones were sequenced;

three were derived from 25S rRNA and one from 16S rRNA. To further confirm that clones not detected in this assay were indeed derived from low copy number genes, genomic Southernns were performed using 36 randomly selected clones as probes. Hybridization banding patterns identified one apparently multicopy gene. However, most appear to be low copy or unique genes. These results also confirm that the clones are of plant origin. To determine the number of contaminating nematode sequences in the library, the replica filters were probed with nick-translated *Meloidogyne incognita* total genomic DNA. One colony gave a signal detectable above background. A second clone encoding a nematode transcript was subsequently identified by genomic blotting.

Dot blots of RNA samples isolated from tomato tissues (galls and whole mature roots from tissue culture, mature leaf from green-house grown plants, and cotyledons, hypocotyls and roots from one-week-old seedlings) were hybridized with probes synthesized from randomly selected giant cell cDNA clones. In these experiments, 5 μ g of total RNA isolated from various tomato tissues was blotted onto nitrocellulose and hybridized with primer extended 32 P labeled antisense probes. Hybridization probes were prepared by primer extension of half of the annealed sequencing DNA template in the presence of α -[32 P]-dCTP. The specific activity of these probes typically was 2×10^9 dpm/ μ g. Filters were probed using standard conditions (Wahl et al. *Proc. Natl. Acad. Sci. USA* 76:3683-3687 (1979)). The presence of equal amounts of target RNA in each dot was confirmed by probing with ribosomal sequences. The exposure times varied significantly between the different filters. This variation is indicative of differences in transcript abundance because the specific activities and amount of probe used in each experiment was essentially the same.

Results from these experiments are summarized in Table 1 (clones which were not sequenced and which gave

no blot results have been omitted). Sixteen probes failed to produce a detectable hybridization signal to any of the RNA samples, suggesting that these cDNAs represent low abundance messages. The remaining cDNA
5 clones hybridized to various subsets of the RNA samples.

Table 1. DNA sequence and RNA dot blot analysis of giant cell cDNA clones

DB#	SEQ. ID. No.	Identity ²	Tissue source of RNA ¹					
			G	D	L	H	A	R
101	SEQ. ID. No. 1	Pioneer						
102	SEQ. ID. No. 2	Pioneer						
103	SEQ. ID. No. 3	16 kD E ₁ enzyme	-	-	-	+	+	-
107	SEQ. ID. No. 4	Peroxidase	-	-	-	-	-	-
108	SEQ. ID. No. 5	Pioneer	-	-	-	-	-	-
110	SEQ. ID. No. 6	Pioneer						
111	SEQ. ID. No. 7	Pioneer						
112	SEQ. ID. No. 8	Pioneer						
113	SEQ. ID. No. 9	Pioneer	-	-	-	-	-	+
114	SEQ. ID. No. 10	Pioneer	+	-	+	+	+	-
115	SEQ. ID. No. 11	Pioneer	+	-	+	+	+	-
117	SEQ. ID. No. 12	RNA pol II Heptamer repeat						
118	SEQ. ID. No. 13	Pioneer	-	-	-	-	-	-
119	SEQ. ID. No. 14	Pioneer	-	-	-	-	-	-

¹RNA samples from the tissues indicated (G: gall; D: RNA isolated from cultured, uninfected roots, and used as driver for the subtractive cloning; L: leaf; H: hypocotyl; A: cotyledons plus apex; R: primary root from young seedlings) were probed with anti-sense probes from the cDNA clones: + indicates a signal was detected, - indicates no signal was detected, no entry indicates that the clone was not tested.

²Putative identity of partial cDNA clones based on DNA or deduced amino acid homology with sequences in GenBank or PIR. Clones with no meaningful homology were termed pioneers.

122	SEQ. ID. No. 15	Extensin- like pioneer	-	-	-	-	-	-
124	SEQ. ID. No. 16	Pioneer	+	?	-	-	-	-
131	SEQ. ID. No. 17	Receptor kinase homologue	+	-	-	-	-	-
132	SEQ. ID. No. 18	Anti- integral membrane protein	+	-	-	+	-	-
133	SEQ. ID. No. 19	Zea repetitive element/cyc lophylin 3'	+	-	+	+	+	+
134	SEQ. ID. No. 20	Pioneer	-	-	-	+	-	-
136	SEQ. ID. No. 21	16 kD E ₂ enzyme						
137	SEQ. ID. No. 22	Pioneer	-	-	-	+	+	-
139	SEQ. ID. No. 23	Pioneer	+	-	+	-	-	+
140	SEQ. ID. No. 24	Pioneer	+	-	+	-	-	+
141	SEQ. ID. No. 25	Pioneer	+	-	-	+	+	-
142	SEQ. ID. No. 26	anti-Ef-3	-	-	-	-	+	-
144	SEQ. ID. No. 27	Ribosomal protein L38						
146	SEQ. ID. No. 28	Pioneer						
147	SEQ. ID. No. 29	Pioneer						
148	SEQ. ID. No. 30	Pioneer						
149	SEQ. ID. No. 31	Pioneer						
151	SEQ. ID. No. 32	Pioneer						
152	SEQ. ID. No. 33	Pioneer						
153	SEQ. ID. No. 34	Anti- ripening associated membrane prot						

154	SEQ. ID. No. 35	Pioneer						
155	SEQ. ID. No. 36	Pioneer						
156	SEQ. ID. No. 37	Pioneer						
157	SEQ. ID. No. 38	Pioneer						
161	SEQ. ID. No. 39	Pioneer	-	-	-	-	-	-
163	SEQ. ID. No. 40	16 kD E ₂ enzyme	-	-	-	+	+	-
164	SEQ. ID. No. 41	Pioneer	-	-	-	-	-	+
165	SEQ. ID. No. 42	Pioneer	-	-	+	-	-	-
166	SEQ. ID. No. 43	Pioneer	-	-	+	-	+	-
168	SEQ. ID. No. 44	Mucin						
169	SEQ. ID. No. 45	Novel 16 kD E ₂ enzyme						
172	SEQ. ID. No. 46	L38 ribosomal protein						
173	SEQ. ID. No. 47	Pioneer	+	+	+	-	-	+
175	SEQ. ID. No. 48	Pioneer						
176	SEQ. ID. No. 49	Pioneer						
177	SEQ. ID. No. 50	Proline-rich wall protein						
178	SEQ. ID. No. 51	Pioneer						
179	SEQ. ID. No. 52	Pioneer						
181	SEQ. ID. No. 53	Transmemb rane turgor- responsive prot						
182	SEQ. ID. No. 54	Pioneer						
183	SEQ. ID. No. 55	Pioneer						

187	SEQ. ID. No. 56	Pioneer						
197	SEQ. ID. No. 57	Pioneer	-	-	-	-	-	-
198	SEQ. ID. No. 58	Pioneer						
199	SEQ. ID. No. 59	anti-Ala tRNA synthase	-	-	-	-	+	-
201	SEQ. ID. No. 60	Pioneer						
203	SEQ. ID. No. 61	Pioneer	-	-	-	-	-	-
205	SEQ. ID. No. 62	Pioneer						
207	SEQ. ID. No. 63	Pioneer	-	-	-	-	-	-
208	SEQ. ID. No. 64	Pioneer	-	-	-	-	-	-
209	SEQ. ID. No. 65	Pioneer						
210	SEQ. ID. No. 66	Pioneer	-	-	-	-	+	-
212	SEQ. ID. No. 67	Pioneer	-	-	-	-	+	-
214	SEQ. ID. No. 68	Pioneer	-	-	-	-	-	-
215	SEQ. ID. No. 69	Zn-finger domain	-	-	-	-	+	-
216	SEQ. ID. No. 70	Pioneer	-	-	-	-	-	-
217	SEQ. ID. No. 71	Laminin B receptor	+	-	+	-	-	+
218	SEQ. ID. No. 72	Pioneer						
220	SEQ. ID. No. 73	anti-PEP- carboxylase	-	-	-	-	-	-
221	SEQ. ID. No. 74	Pioneer	-	-	+	-	-	-
222	SEQ. ID. No. 75	Pioneer	-	-	-	-	-	-
223	SEQ. ID. No. 76	Pioneer	-	-	-	-	-	-
224	SEQ. ID. No. 77	Pioneer	-	-	-	-	-	-

226	SEQ. ID. No. 78	Proton ATPase	-	-	-	+	-	-
227	SEQ. ID. No. 79							
228	SEQ. ID. No. 80							
230	SEQ. ID. No. 81							
231	SEQ. ID. No. 82							
232	SEQ. ID. No. 83							
233	SEQ. ID. No. 84							
234	SEQ. ID. No. 85		+	?	-	+	+	+
236	SEQ. ID. No. 86							
239	SEQ. ID. No. 87	eF 11e 5'UTR	-	-	-	+	+	-
240	SEQ. ID. No. 88	Pioneer	-	-	-	+	+	-
241	SEQ. ID. No. 89	Pioneer						
244	SEQ. ID. No. 90	Pioneer	-	-	+	-	+	-
246	SEQ. ID. No. 91	Pioneer						
247	SEQ. ID. No. 92	Pioneer						
249	SEQ. ID. No. 93	Tob RB7- 5A homologue						
250	SEQ. ID. No. 94	Pioneer						
252	SEQ. ID. No. 95	Pioneer	+	-	-	+	+	+
255	SEQ. ID. No. 96							
256	SEQ. ID. No. 97	Pioneer						
263	SEQ. ID. No. 98	Pioneer	-	-	-	+	+	+
264	SEQ. ID. No. 99	Pioneer						

265	SEQ. ID. No. 100	anti-Tnt1-94 transposon	-	-	-	+	+	+
266	SEQ. ID. No. 101	Pioneer						
275	SEQ. ID. No. 102	Pioneer	-	-	-	+	+	-
277	SEQ. ID. No. 103	Pioneer						
279	SEQ. ID. No. 104	Pioneer	-	-	-	-	-	+
280	SEQ. ID. No. 105	Myb DNA- binding site	-	-	-	+	+	-
288	SEQ. ID. No. 106	Pioneer						
289	SEQ. ID. No. 107	Pioneer						
291	SEQ. ID. No. 108	Pioneer						
L23762	SEQ. ID. No. 109							

Only one clone (DB#173) produced a signal in the RNA from mature roots. This is important because mature root was the source of the RNA used as driver in construction of the subtractive library, and provides strong evidence that the subtraction was effective. Fifteen of the cDNA clones detected transcripts in seedling root (Table 1), and presumably encode functions associated with young, expanding roots. Three of these appeared to be root-specific.

Despite the fact that only cDNA synthesized from giant cell mRNA was exposed to the vector thereby ensuring that all clones in the bank must encode giant cell transcripts, most probes also failed to detect transcripts in gall RNA. Although this is partly due to giant cells representing only a small fraction of the total mass of the gall (it was not technically feasible to collect the numbers of giant cells required to isolate sufficient RNA for blot analysis), it also suggests that the clones in the bank do not encode abundant transcripts. Ultimately, the (elevated) presence in giant cells of transcripts defined by each clone in the bank can be confirmed using, for instance, *in situ* hybridization.

Although different clones reveal a range of expression patterns, many detected transcripts in RNA isolated from hypocotyls and/or cotyledon plus apex tissue, generally at levels much higher than in uninfected seedling root. Ten cDNA clones detected a signal in leaf RNA. Overall, these results give a picture of giant cells sharing transcripts with actively dividing and expanding tissues, and also non-root tissues.

DNA sequencing

Partial sequences of each clone listed in Table 1, above, are provided in the Sequence Listing, below. The Sequence Listing also includes the complete sequence of one clone, SEQ. ID. No. 109, which encodes a ubiquitin carrier protein. Reflective of the directional nature of

the cloning, each sequence began with a poly-T tract (ranging in length from 4 to 75 residues), corresponding to the poly-A tail of the transcript. Each sequence was read only as far as the first ambiguity, including
5 potential compressions. Thus, although the sequences represent readings from one strand only, we believe the degree of accuracy to be high. The presence of a long oligomeric tail rendered some clones unsequencable. Four independent rRNA clones from the same bank also were
10 determined. The sequences (not shown) corresponded exactly to those published for tomato (Kiss et al. *Nucl. Acids Res.* 17:796 (1989)). This suggests also that the number of PCR-introduced artifacts in the bank is low.

Sequences were compared to others in the public domain
15 DNA and protein databanks using the BlastN and BlastX algorithms (Altschul et al. *J. Mol. Biol.* 215:403-410 (1990)). With some exceptions noted below, only those database matches involving homology with the correct strand and in the correct part of the matching gene
20 (i.e., the 3'-end) were considered, and a score of at least 100 was chosen as indicating a potentially valid homology. Most of the cDNA sequences failed these tests, and are listed as "Pioneers" in Table 1. Four clones were determined to share sequences with genes previously
25 cloned in tomato, all other non-pioneers shared sequences with sequences from other species.

By isolating and characterizing full length cDNA clones, including *in situ* localization to giant cells the identity of the DB#103 transcript was confirmed as
30 encoding an E₂ enzyme, a key component of the protein ubiquitination pathway.

The DB#163 cDNA is identical with the DB#103 sequence, but has an additional 19 residues immediately before the poly-A tail. Because the gene encoding these
35 transcripts, *LeUBC10*, appears to be unique, the different 3'-ends might arise by differential RNA processing.

Computer translation of the DB#117 cDNA revealed a hypothetical protein with multiple contiguous repeats of a seven amino acid motif, shown aligned in Figure 2, and terminating with a stop codon 47 bp 5' from the poly-A
5 tail. This motif is strikingly similar to the motif TSPSYSP, a structure diagnostic for the carboxy terminal domain (CTD) of the large subunit of RNA polymerase II. *Arabidopsis* has 40 copies of this repeat (Dietrich et al. *Plant Mol. Biol.* 15:207-223 (1990)) and *C. elegans* has
10 42 (Bird and Riddle *Molec. Cell. Biol.* 9:4119-4130 (1989)). Although not previously cloned from tomato, it seems likely that DB#117 encodes this gene. Southern blotting (not shown) suggests that the DB#117 region is unique.

15 BlastX analysis revealed significant homologies between the inferred DB#280 product and different members of the *myb* gene family (Fig. 3). Homology is highest with the DNA binding domain of the petunia *myb Ph3* gene product, although multiple alignment with Mybs from other
20 plants and vertebrates revealed that this homology extends further. As nuclear transcription regulators, members of the Myb family play pivotal roles in the regulation of cellular proliferation. Through interactions with other trans-activators (e.g., members
25 of the Ets family) Myb proteins effect growth control and oncogenesis.

A BlastN search revealed striking homology between the DB#226 sequence and the 3'-end of the *pma4*-encoded isoform (Moriau et al. *Plant Molec. Biol.* 21:955-963
30 (1993)) of a plasmalemma H⁺ATPase from *Nicotiana plumbaginifolia* (Fig. 4). The DB#226-gene appears to be different from those encoding two previously cloned tomato isoforms (Ewing et al. *Plant Physiol.* 94:1847-1881 (1990)). The high degree of homology between the 3'
35 untranslated regions (UTR) of these genes (the tobacco stop codon, and presumably also the DB#226 terminator, is

a further 60 residues 5') might indicate a biological role for this part of the sequence.

Other sequences in the giant cell cDNA bank, including a number of the pioneer clones, encode recognizable structural motifs. For example, part of the DB#215 sequence specifies a zinc finger domain. Additional homologies have been observed in the UTRs of some genes. The 3'-UTR of DB#239 contains a (GCC)₅ element previously noted in the 5'-UTR of human general transcription factor TFIIE (Sumimoto et al. *Nature* 354:401-404 (1991); sequences such as these may play a role in translational regulation.

Four clones in the cDNA bank (DB#142, DB#199, DB#220, DB#265) have high degrees of homology with sequences in GenBank (Blast scores of 246, 499, 806 and 173 respectively) but to the anti-sense strand. These sequences terminate with a poly-A tail, suggesting that they do not represent artifactuary cloned sequences. Significantly, when used as probes in the dot blot assay, DB#142, DB#199, and DB#265 detected transcripts in plant tissues (Table 1). The DB#265 transcript, which encodes a sequence with anti-sense homology to the tobacco retroviral-like transposon Tnt 1-94 (Grandbastien et al. *Nature* 337:376-380 (1989)), and also the *Arabidopsis* copia-like element (Voytas and Ausubel *Nature* 336:242-244 (1989)), appears to be particularly abundant in seedling root tissue.

The cDNA clone DB#249 as a query revealed that its inferred product shares homology with that of the RB7-5A gene from tobacco (Yamamoto et al. *Nuc. Acids Res.* 18:7449 (1990)). Significantly, this gene is strongly up-regulated in nematode-induced, tobacco giant cells.

Taken together, these data show the subtracted library contains bona fide cDNA inserts with a low level of contamination by high copy or nematode sequences, as well as a high degree of complexity.

The above examples are provided to illustrate the invention but not to limit its scope. Other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended
5 claims. All publications, patents, and patent applications cited herein are hereby incorporated by reference.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE REGENTS OF THE UNIVERSITY
OF CALIFORNIA

(ii) TITLE OF INVENTION: NEMATODE-INDUCE GENES IN TOMATO

(iii) NUMBER OF SEQUENCES: 114

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Robbins, Berliner & Carson
(B) STREET: 201 N. Figueroa Street, 5th Floor
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: US
(F) ZIP: 90012-2628

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Berliner, Robert
(B) REGISTRATION NUMBER: 20,121
(C) REFERENCE/DOCKET NUMBER: 5555-316

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 977-1001
(B) TELEFAX: (213) 977-1003

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..210
(D) OTHER INFORMATION: /standard_name="DB# 101"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
ACACGATCAC ATACCAGAGG GCAGACAACC AAGCTGAGAG GTCAAGTGGG TCTGGGAGTT    60
CAATTTCCAA GTCTATGAAA ACCAGTTCTT CAACAAGTTC CGGTGCTGAT CCTTCATTGG    120
TTCAAGCATC ATTGTTAGAT AGTATATTGA GGGAGAACCT CTTGTGATCT GGAGAAAGTA    180
ACCTATTACA GTATTTTGTA CCTCTTACGT                                     210
```

(2) INFORMATION FOR SEQ ID NO:2:

44

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..211
(D) OTHER INFORMATION: /standard_name= "DB# 102"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CATAAACCTG TTTTCTCTT TCCCCCTAT GATGAATCCA GTCTATGAAG TAATGAAAG	60
GAGATTCTGG GAAGGCAGGT ACTGTGTGTG GTTGAGATGG CTTGTGGTTT TAGCAGTGAC	120
TTTTGTTGCA TTGGCGGTGC CCAATTGTTG CTGATTCTTT CACTGTGTGG GAGCAGTGTG	180
TGCATTGTTT TGGGATTTGT GTTGCCTTCT T	211

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..257
(D) OTHER INFORMATION: /standard_name= "DB# 103"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AACTGGCAAA CAAAGTAGAA TTACATTGCA GTTCTCCCT TACTAGTCAT CAAATAAATA	60
TTACAAAATT GAAAACAGCT GTTCCCTTAA CAACCCTCAT GAAGGGAGAT TAAGAAGTAA	120
CTAAGTTCTT TCACGGAATT TATTCAATCA CCCCAGCAC ATAAGACATT GCTGTTACAA	180
AGTCCCAGAC ATGCCTGGAG ACATTTTGGC CATCATCCCA TTGCATATTT CTGAGTCTAG	240
CTACGAGCAG TGGTTTC	257

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: /standard_name= "DB# 107"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGGTCAAAT TTGGAATTGC AGTTTGCTCA CTTGGCCCTC CTGCTGATCC ATCTAGCAAC	60
ACTGAACCAT CACACCCCTG AACAAAGCAA TCGTGGAAT GAAGACGAAG TAAGCCAGCA	120
GCTTGGCCAA CATCATCCTT GATTGTTTT TGAAGCCTGT TTCTAATAAT GGATTCAAGT	180
TGAGGACAAC TAGATTGATA AATGACCATG AGACCTTAGT TAGCAGCCTT GAGCTCCGA	240
TCAAGATTT	249

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: /standard_name= "DB# 108"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGATTACTG AGGTGGTTTT GGATCTTCT TCCGGCCTT CGCTATATAC ACAAGATAGG	60
ACAATGATCA GTAGTTGTTT GTTGTTGCC TTGTCTGA GACTTTTGTC ATGTTAATGG	120
GGTTTCCAAT GC	132

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

46

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: /standard_name= "DB# 110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCAGTCCCT TTGGGTGTCA CAATTTTCTC AGCACTTGAA CTCAAGCCAT TAGGATCAAT	60
GTTATTCCT CTCTAATAG CTGGTAGTCT TGGCGACTTC ATTTTGTTGT CGTGCTTTA	120
GATCTGTAC ATATTAGCGG CTTTCTTTT GTAGCATCTC AGTTAGAAAG TACTGGACGT	180
GCCTTTTCTT TGCGCAGCAT AAACACG	207

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..256
 (D) OTHER INFORMATION: /standard_name= "DB# 111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAATTACACC CATTATCA ACCTTGAGT AAATCTTACC AGCACTAAAC TGGCTTACAA	60
TGCCATGGGC AGTTCGCTCA ATAACAATTC ATCTAAAACA TTTTGAAGG CACTGTGCTA	120
ATGTTTCTAA CACATAAAAT TGAATCTAAG GTCCAAAATT TAGTTTTCAT TACAGAGGCA	180
GCCAAGAATG CAAACAATA CCAACCATGC ATTTGCATGA CTGTGGATCT TCAACTTCAT	240
CTCACAATA ACGCAT	256

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..179
 (D) OTHER INFORMATION: /standard_name= "DB# 112"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTATGTTGT ACGTGCTGT TGAAGTTGAA GATCTGAAGA TCGTTTGCT GCTGTTGGAA	60
GTAAATCAT TTTGGTCACA CTGTTGGGTT GTTCCTGTTA CATTTGGAAA CACTCAACTT	120

TTAACTCCTA AACCTGTTGC TGTGCTTGT CTGAATCTGT CGTGTGCATC ATTAACACA 179

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..210
(D) OTHER INFORMATION: /standard_name= "DB# 113"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTTAAAGCT AGTCTTCTT AGGTTACAT AGCAGTTACT TCCAAAAGTT AAAACATAAA 60
TCAAAATTAT CCCATTACAT CATTTAACTG AAGGGAGATG CAAATCAAAA AGCTCTAATG 120
CCATATGTCT TCTACCAGCA CCAATGTAG AGGTCCTCGT AGAAACTCGT ATTCAAGATT 180
TTTAACGGTA CTTGATGAAG CCAATTCCTT 210

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..110
(D) OTHER INFORMATION: /standard_name= "DB# 114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGGAGGTTTA TCTGATACAG TTGACTTGAA ATATGGCATA TTGGGTCTTA AGCCAACATC 60
TGCTTCAGTC ATCTTATCCA AACTGACTT GACAAGTTCA ACATTTCCG 110

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

- (ix) FEATURE:
(A) NAME/KEY: misc_feature

(B) LOCATION: 1..223
(D) OTHER INFORMATION: /standard_name= "DB# 115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAGCTCAACT AGTCGAGCTA GTAAGAAGAG AGATTATAAT TGTAATCA CTCACCAATA	60
CTGCTATTAT ACACACCAA TGTAAGGCAA ATATAAGAAT TCATTATTT AGCTTCTTCT	120
GGATCTACTT TGATAGAAAG CGCAGTGGTA CATGGTGGAT GAGCAAGACG AACATACTT	180
CAAAGAAGAC CATCATGAAA GTTGTGACA TGCTTTAATC AGT	223

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc feature
(B) LOCATION: 1..279
(D) OTHER INFORMATION: /standard_name= "DB# 117"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTAACCACCG TCGTATTTTC CGCCGATACC CATCGTCGTA GCTGGGCTTA TAACCTGTCG	60
TAGCTTGGCT TGTAATTGTC ATAGCTAGGC TTGTAAGTGT CGTAGCTTGG CTTGTAATTG	120
TCATAGCTAG GCTTGTAAGT GTCGTAGCTT GGCTTGATC CGCTGTCGTA GCTAGGCTTT	180
TTGTAACCAT TGTCGTAGCT GGGCTTGAT CCGCTGTCGT AGCTGGGCTT TTTGTAAGTA	240
TTGTCATAGC TGGGCTTGTA GCTGCTGAG CTGGGCTTT	279

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..267
- (C) OTHER INFORMATION: /standard_name= "DB# 118"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGAGTGAAAT CTTCAAATA GCAGTAAAT TGGTACCTTC ACTATACTG GTGTTTCATA	60
TTTTTCTTAG CTAGATGCA GTTGATTGT TACAACAAAT ACTGAGTTAA TGAGGCCTTG	120
TAGTAGTAAG TTGGGACCAA ATTGGATTTC TCATCATTAG ATTGTTTGTG CAGTTACTAC	180
CTTCAGGTAG ACAAATATAC TTAGTAAGAG GAGAAACCAA TGGAAGAGAA GGTGATTGTA	240
GCCATGGTTA GGGCATGTTT CTTGGCT	267

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: /standard_name= "DB# 119"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACCTACCACC TCCCACCGGC AATAGGTACA GTCCACCAAG GCTAGGACAG ATGGAAATAA	60
CTACCTAGTG TTTTCTTGTG TCCGCTAGAA ACAAATTAG CTAGTTTCA TCTTCAAGAT	120
CCAAACAAAG GCAGTAAGCA ACTAAGCCAC AACTGAACAT ATCTGAGATA TCTCACTATG	180
TCAGCCTTAT CTTCTGGT	199

(2) INFORMATION FOR SEQ ID NO:15:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 303 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..303
(D) OTHER INFORMATION: /standard_name= "DB# 122"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGGGTGAGGT GGTATTTGAG GATTGGGGTT TTGAGGAGGT GGTGGGATGT GGTAAGGGGT	60
TGAGGCATAC TAAGGATTTT GTGCAGTCAA GTCTATTACT GAGTGATTCT AACCAGGAGT	120
GGATAGTGCG TTCTTAGCCT ATTCTATGTT TGAAGAGGGA AAGTGTGTA GAGGCCCTCC	180
ATCAGTATTA GTGTTGGCAG TAAACCTAA TGGAGGCAGA TCCTGTCTCT TTGCATTCC	240
ATTCTCATCT CAGTGATCTG CTGCATTAAC TGTATAATCT GTTCATTCTG ATCTGCTATA	300
GTG	303

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..196
(D) OTHER INFORMATION: /standard_name= "DB# 124"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGAGGATA TCCATTTGTG AGCAAAGCAT CAACTTACA ATTGATTACA TAAGAAGCTA	60
TGTGTCAAAC TGCTGAATCT AAGAAAGTGG TACTCGATTG GGAGTTGAGG ATATGACAA	120
GAATTAAACC TGTTAGATGT AAATCTGCCT AGTAATTCTA TGAATTACCG ATAGTTTGAA	180
TTGGACAAGT TAGACT	196

51

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 272 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..272
(D) OTHER INFORMATION: /standard_name= "DB# 131"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAAGGCTTCA CACTGAGCCA TGAAGTTCTT AGAAGTAGCC CCTTGTGTTT CAATGTTTAT	60
CACCTTCACC GCAACCATAC ATTCACCTGG ATCAAGTACC CCTTTGTAAA CAGAAATAAA	120
GCTACCATTT CCAATCAAAT TGGCAGAAGA GAATCCATTT GTCGCTCTAT ATAGGCTCTC	180
ATAAGTAACC GGTGAAGATG TTAAGAAGG ATCTCCCTTG CCTTCCTTAA CCGAATGATT	240
ATGACTAAGC ATGATGAAAC CATGCACAGT CC	272

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..164
(D) OTHER INFORMATION: /standard_name= "DB# 132"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGGTCATGAC CGAATTGGCT CTAATTGGGG CTGATATTCA AGAGGTTATT GGAAGTGCTA	60
TTGCTATAAA GATTTTGAGT CGAGGGTTCT TGCCTCTATG GTCTGGTGTT GTCATCACTG	120
CTCTTGATTG CTTTGTTATC TTATTTCTTG AGAACTATGG ATGA	164

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(xi) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..348
- (C) OTHER INFORMATION: /standard_name= "DB# 133"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AGCAAGTCTA TGAGTATCTT ATTTAATTGT AGTCTTAAGA TTAAACATAA ACTGGTGGTG      60
CACCAGCTGG TCGTGTGGTG AACGAGACTT TGGATTTGTC CATTATGCAG AAAGGTCGAG      120
CGCTCTGAAA GCTGTCAAAG ACACTGAAAC ATATGAAGTA AATGGTCAGA TGTTAGAAGT      180
AGTTCTTGCA AAGCCTCAGA CTGAAAAGAA GTTTGATGCA GCTAGTCCTC ACATGCGATG      240
CCACATCATA TTATATTCCT ATCCAGGCTA TGGTGACTTC CGATGACCGA TGTACCTAT      300
CTGCTGGTAT GGTGTCGTCG GTCGTCGTCG TCCGCGTCGT CACACACC                    348
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: /standard_name= "DB# 134"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
AACCCATCAA AAAGTGATT TATATCTCAG TGAACATATG TTCAGCACTC GTGCTGTCTG      60
ATCTAGGGCC AAAACTGGCA CAGGTACAAC CTGCAATACC TCATTACAAC ATTTGAGAAA      120
TGAGCAAATA ATACTTCCAC ATTCAGCATA AACAAAAGTT ATCTTGACGT TGATCTGTTT      180
AAGATGAGAT GATGATCTGT TTTTCTCAGC CAATAGTGCT CAGCATATCT TCTTCATCA      239
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..255

(D) OTHER INFORMATION: /standard_name= "DB# 136"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCAAACAAA GTAGAATTAC ATTGCAGTTT CTCCTTACT AGTCAACAAA TAAATATTCA	60
CAAAATTGAAA ACAGCTGTTT CCTTAACAAC CCTCATGAAG GGAGATTAAG AAGTAACTAA	120
GTCTTTTCAC GGAATTTATT CATTACCCCC AAGCACAATA AGACATTGCT GTTACAAAAG	180
TCCCAGACGT GCCTGGAGAC AATTTTGGC ATCATCCCAT TGCATATTTT TGAGTCCAGC	240
ATCGAGCAGT GGTTT	255

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 283 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..283

(D) OTHER INFORMATION: /standard_name= "DB# 137"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AATAATCCAA TAAATACAG ATTGGAAGTT ACATTACAAT CCCAAATGAC ATGATATTAT	60
ACGTTTCATCA AACAACTCTAT CCACAAGAGA AAACAACCAA AAGCCAAGAA TAAATGGAAA	120
AAGTAGCTAG GTACTCCATT AGCGAAGTAG TAATAATATG GTCTTCAAAT ATCCACCATA	180
TGATGATCCA CTGGGTGAGG ACCAAATAGC ATAAATGATA CCAGGTAGCT ACCAAAGAGA	240
GCAGCAAAC TGATGTTTTT GGCTATGGAA TCATGCTTGG AAT	283

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..243

(D) OTHER INFORMATION: /standard_name= "DB# 139"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAATTGTC CTACAACTGC ATTGCACAGA AGAGTACAAT TTTTCTCTC TGAAATTAT	60
TACACCTCAA GTAGTCCAAG TCCAGGCAGG ATCATCAGAT GTACAAAGAT TTGCTCAGTT	120
TTGTTCTCTCC TAATCAATTC AAAGGATCTA ACTCAAACT TGGCGTTGCA ATAGATAAAT	180
GCTGCTGGAT AATTAGGATA CAACATATCT AGTGTAATCC CACATAGGTC TGAAGGGTG	240
GTT	243

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..223
- (D) OTHER INFORMATION: /standard_name= "DB# 140"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACTTGAGAA CGTTAATATA AAAGGTAAAT GATTGTGTT AAAATAATTT TACGTCTGGA	60
TAGCTTTTTA TACAAGATTT TGGAGTTGCT TCTCCTTAAA TCATATTAAG GAAAGACACA	120
CCTCCAAAAC ATTCTCTTGG AAGAAATACC AATTGAAACA CATTACACAT ACTGAGTTGA	180
GGGTCTTGTA ATAGGCATCA GTTAGGTCA GGATAACGAG TTT	223

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..163
- (D) OTHER INFORMATION: /standard_name= "DB# 141"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTTATTTAT GTCTGGTGTT TCCTCTAAAC CTTGGGTAAT TGCTGTAACC CAGTACGGCA	60
GTACCTGCAG TTTTCTTTA TCATATGATC TTATTATGTG GCACAGCAA CGGCCAGCCC	120
ACCGAAGCCG GCGCTCAAC CAGGATCATC TATGGAGGAA TCT	163

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs

55

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..206
(D) OTHER INFORMATION: /standard_name= "DB# 142"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTCAGCCTA CTCTATTGTT GTTGGATGAA CCTACAAATC ATCTTGACCT TCGGGCTGTT	60
CTATGGTTAG AGGAGTACTT GTGCAGATGG AAGAAAACCT TGGTCGTTGT TTCGCATGAT	120
CGAGACTTTC TGAACACTGT TTGCGGTGAG ATTATTCATC TCCATGACAT GAAACTACAC	180
TTCTATCGTG GTAACTTTGA GATTTT	206

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..309
(D) OTHER INFORMATION: /standard_name= "DB# 144"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGGGGGCAA CACAATATCT AGAATGAACA AAACTTTAGA TATTCGACAG GATAAGAAAA	60
TGGTAAAGGA ACATAATAGT TCTACGAATT CTCAAGTATC TTCTAATCAT CTAGGGGGAA	120
GGGGCACATT AACTCTTCCA TCTTCAAGGT CTTGGACGCT CAAACCTGGA GGAAGTGACT	180
GCTTCAACTT GTCAGCCTTC TCAAAGTCCA GCACACAGAG TGTGTAAGG TACTTGGAGC	240
CAGCGACCTT GAACTACCA TATCCTTGT CTCTGATCTG CAGTCGTGCA TCCTCCTCCT	300
TGCTGTAGG	309

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..292
- (D) OTHER INFORMATION: /standard_name= "DB# 146"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTGTGAGTT AGTTTTTGT GGTTTTCATG AATGCCGTGT CAAGGAGACC TTAGATTGT	60
GTTTGGACAG TTTCATCGAG TCTAAAGCAT CGAGTATATT GATTTCCTTA TGCGGTTGT	120
GTGTACCGGA TTCCGAACGA ATCCTGAGGG TCCTCTTGAT GTTTTGAAG TTGGCTGATT	180
TTTCTGGTGC CTGAATCTAG TGTGTCTCGC GATCTCGAGC CTCATTGTTG CGAGGTAATG	240
TTCGCTTCGC GAAGGGGTCA AGTTCCTGAT CTCACGTACA CAAGAAGGAC CT	292

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: /standard_name= "DB# 147"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGCCCTAG GCCACCATCC TTCTTAAAGT AAAGGAAGAA AAGAGGAAGA AGATTGCTAA	60
GAACTTGAAG AAGTACAGCA AGAAGTATGA AGCAGAGGAT CAGGATGTTT CATTGCTGTT	120
GAGCGAGCAA GACCGTGAGA AGCGAAAGAA GCTGAAAGAG ATGGGAGCAT GGATTA	176

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..184
- (D) OTHER INFORMATION: /standard_name= "DB# 148"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAGATGATTA AGCTAAATAT CAAATAGAAA CCAAATCCAT AGGACATATA TCTTTTAAAC	60
AGCAATAATT CCAATCTAAC AGATGAGAGG TAATATTCCA GAAAAAATA TTCGAAACTT	120
CGATTTCATCA GCGAAATGAA AGACATCAAA CGAAACAGTG TCAAACTGC TTCTTTAGAA	180
ACGT	184

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..325
- (D) OTHER INFORMATION: /standard_name= "DB# 149"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ACCGTTCATT TTGGAATCGT AGCACAAAAC CTTCTTTGGA TCTCGGAAG GAGCTCCTAG	60
ATCTTTTTAG TGCAATAAAA ATGGCGAAAC GCTTTTTTTT TCACAAACAG CGGATCAGAA	120
GCCAAATGACA CACAGGTGAA ACTGGTATGG TATTACACAT GCACTCGGCC AGACAAAAG	180
AAATTTATTG CTCGAACAAA ATCATACCAC GGATCCACCT CTCATTTCGG CTAGTCTCTC	240
TGTCTTCTG CACTACATCA GCAATTCGAT CTACCAGCTC CGTTTGTCTG CATACTGACT	300
GCCCTATTTG GCGCTTCATC AGCCA	325

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: /standard_name= "DB# 151"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGACTACAAA CTTTGTATGC TCTATTCC	60
TTAACAAGGA CAGTTTGT CAACTAAAT ATCCTTGATC CATCTGTCAT GAAAGGATCT	120
GAAAATACCA TTGATTCAGC AAAAAGTACA CAAAGGACAT ATACTAGCAA TAAAGTTGC	180
AGGAACACAT ACTGCCGTCA AAGAGAGTTC AGGCCAGCGA CATTGTTCTA TTAATCCTAC	240
TGGTATCCC	249

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: /standard_name= "DB# 152"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACCTAAATG AACCTCTAGC TTAAGATAAA CAGTTGAACA TCACCAGATA ACGAAAATAC	60
CGGCGAAACG ATAGGAGTTT AGTCAAGCCA AAAGTATTAT TATGGATAGC AAATAATCAG	120
GACAGTGATC TACTACTATG TCTTTGCAAG AAAAACTGT TGCTACAAAC TATAATTACT	180
AACCGGTCTA CATGTAGGGT TGATAGGCTG T	211

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..302
 (C) OTHER INFORMATION: /standard_name= "DB# 153"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTGGTATGA TCTTTGCTTT GGTCTACTGT ACTGCTGGTA TCTCAGGAGG ACACATTAAT	60
CCAGCTGTGA CATTGGTTT GTTCTTGGCA AGGAAGTTGT CATTACAAG GGCAGTGT	120
TATATAGTGA TGCAGTGTCT TGGTGCTATC TGTGGTGCTG GTGTTGTGAA GGGTTTTATG	180
GTTGGACCCCT ATGAGAGACT TGGTGGTGGT GCTAATGTTG TTAATCCTGG TTACACCAA	240
GGTGATGGAC TTGGTGCTGA GATTATTGGT ACTTTGTCCT TGTTTACACT GTTTTCTCTG	300
CC	302

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: 1..243
 (D) OTHER INFORMATION: /standard_name= "DB# 154"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGATTAGGTG ATAGATATGA ACCCTAGAAA TAGGGGATTT TTGGCTAATT CAATTGAAAG	60
ATTGATTAGA GATCAAATTA AGGAGATCGG AGTATGTAAG GCAAGCAGTG CAAGAGGACA	120
ATGGTGGAAA CTATGCAAAG GCATTTCCGT TGTATATGAA TGCAATCGGAG TACTTCAAGA	180
CCCATTTGAA GTACGAGAAG AATCCTAAGA TAAAGGAGGC AATTACCCAG AAATTTACTG	240
AGT	243

60

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: /standard_name= "DB# 155"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGCTGATTA AACCTTCCAG TGATGGAAAT GCTGGTCCTG AGTTGGTTAA AGGGAGTAGA	60
AAGTCACAGA TGCGAGGAAG ATGGAGAGGG ATTGACCCAA TATTATTTTA CCACGAGGAG	120
ACAACAGTGG GTCAGATAAA GGCCTTCTAT GGCATTAAGG AATCCTTTCC ATTCAAAGGT	180
CATTTGATTG TGAGGAATAC TGATATCGAC CATGTGAAAA GAGTTTATTA TGTATCTAAA	240
TCTGTGAAAG AAGTTCCTAA ACTCAATTTT GT	272

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: /standard_name= "DB# 156"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACCAGAAATG CAGATTGGAT AGAGATGATT CCACAAAGGG AATCTTAATT GAAACAAGAA	60
GATATCCTGT GAATATATTT ACAGATTGAG ATAAGACTTC TATAAACCT CAAAATTCCT	120
CAATCATCTG ACACCTAGCT TACTATTTTA CCTGGTTCGT TCAGCCTATT TATACCAACA	180
AGACCTACAT CTTAAGAAAT TAGAGACAGA TCCTAATAAT TCATCTTCAT ACATGTTATT	240
GACATTGCCG CCATCTCGTG ATTTATCCAA GCAGCAACC	279

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv. 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..183
- (D) OTHER INFORMATION: /standard_name= "DB# 157"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGCTGGTAAC AGAATGAACC AAGGAAGAGA GCAATTTCCA GTCCATAAAT AAAACTAGCA	60
TCAAAATGCC CAACAGCAGA GACCCTAGCT GCCAATAAGA CATCAATTTT CTAATGTTTT	120
GCCTTAAC TAATGTGCCTT TCAGCTGTGA CTTCAAAAAT ACGAGACTCA GGTTCCTTAT	180
GGG	183

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv. 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..290
- (D) OTHER INFORMATION: /standard_name= "DB# 161"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CGAGAGAGAT CCCGGTCTAC AACATCACAT TAGAGAGGTA TTCTCAAATA TACAAAACAG	60
AAACACCCCT CTATCTCTTG AAAGTTTAGC AAGTTTGTTA AATTGCAAGA ATCAGTGCAT	120
GCTTGTGAT AAGTCCTTGA AGATAGCTGC TCAACTTGCT GTTCAACTTG GGGGTAGATA	180
TTAGACATTA TATAGCCTCA TTTCTCTTC GGTGCAATAG TTAGTAACTC AAAGCTCCTA	240
AGAGCATCAT CCTACCCCT CTAGTTGGCA GGTAGCCGCG GTAAGAGTAG	290

62

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..279
- (D) OTHER INFORMATION: /standard_name= "DB# 163"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGGGAAAGGC GAATGTCAAA CTGGCAAACA AAGTAGAATT ACATTGCAGT TTCTCCCTTA	60
CTAGTCATCA AATAAATATT CACAAATTGA AACAGCTGT TCCCTTAACA ACCCTCGATG	120
AAGGGAGATT AAGAAGTAAC TAAGTTCTTT CACGGAATTT ATTCATTCAC CCCAAGCACA	180
ATAAGACATT GCTGTTACAA AAGTCCCAGA CATGCCTGGA GACAATTTTG CGCATCATCC	240
ATTGCATATT TCTGAGTCCA GCTACGAGCA GTGGTTTCC	279

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..172
- (D) OTHER INFORMATION: /standard_name= "DB# 164"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCATGGACAA TATCGCCGAC TGGCGGTCAT TCACAGGGAA CTTTACAGG ACCCAAGAGT	60
TAATTGGTCA GGCTCCAGTC TTGGAAGTGA GGCTACTGGC TACGGATTGG TTTTCTTTGC	120
TCAACTTATG CTTGCAGACA TGAACAAAGA ACTAAAAGGA TTAAGGTGTG CA	172

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: /standard_name= "DB# 165"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AAGGAAAGTT TATGCCCTA TGGGAGCTTT TCGACTGCAG AAACCTACTC AAATTAGTAA	60
TTGAAATGC ATAGCAAGAC AATATCTCAC AGGCCACATA TAGGCCATAA TAACATGTAG	120
TATGTCTTAT TTAAAGAGGC GAACATTAGA ACACT	155

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..262
- (D) OTHER INFORMATION: /standard_name= "DB# 166"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AGCAGCTCAA GTGGCATGTG TAATCTCAAT GTTAATAGTC ACTTATAGTA CTGATTGGGA	60
AGGAGCATCC TTGAAGGCAA AACAACTAGT GGAAGAAGCT AATGAACTCC CATATGAAGA	120
TCAACTGGTA AAAATTGAGG AGGGTAATGG ATTTCTCAAC GATTTAGCTT CTGAAGTGGA	180
AGGAATCTAA GGATGCAATG GATGCAAGGA AAAGGAAGAG ATGGCCACAG CAGAGAACAA	240
GACATTACAT TCTCTCAGTA TT	262

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

64

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: /standard_name= "DB# 168"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTGTGATG GTCCAGACGT GCCTGTTGGT GCTGGTGTG ATGGTCCTAG GCTGACAGTT	60
GGGTTACCAG TAGGTTCAAT TGATAGTTGG GGTGTGCCTG TAGGTGCGGT CGTAGCTTCA	120
GGAGTTCCTG TTGGTGCTGG TGTTGATGGC CCAGGAGTGC CTGTAGGTGC GGTGTAGCT	180
TCAGGAGGTT CCT	193

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: /standard_name= "DB# 169"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GAACGCTTAT AAAGGTGTTG GCATTGTTTT AGTTACTATT TCCAGTTATT GTCCCTTTCC	60
AGCAGAATAT GTTGCTTCTC TCAGGAAATG CAGATATTCG TGAGTCACCA CTCATCATTA	120
GAGCCATCAA CTCAGATTGC AACCTTTTAA GAACAGACTG AGTATCAACC GTCTTCACAG	180
TAGTCTGTGT CTGCTTTGGT GAAGGT	206

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /standard_name= "DB# 172"

65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGGGGCAA CACAATATCT AGAATGAACA AAACCTTAGA TATTCGACAG GATAAGAAAA	60
TGGTAAAGGA ACATAATAGT TCTACGAATT CTCAAGTATC TTCTAATCAA TCTAGGGGGA	120
AGGGGACACA TTAACCTCTC CATCTTCACA GGTCTTGAC GCTCAACCT GGAGGAAGTG	180
ACTGCTTCAA CTGTGCAGCC TTCTCAAAGT CAGACACACA GAGTGTGTAA AGGATCTGGA	240
GACGCGAACC TTGAACCTAA CCATATCCTT GTTCTTCTTG ATCTTGACAG ATCGTGCATC	300
TTCTCTCTTG CTGTAAGA	318

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..239
- (D) OTHER INFORMATION: /standard_name= "DB# 173"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CTTCTTGCT ACTATTGCCT TTTGCGTAG TATGCAAGAG GCAATAGTAG CAAGAAGCAG	60
AGCTGAAGCC CCAACTGATG ATCCTATAAT GATTTTCTTA CGGCTGCGAT TGGTTTCCCC	120
TTCTGAAGA TTAAAGTTTC CAGTATAATT CAAAATCACA CCGTTATCAC GAAGACCAGA	180
TGTCCCAACT TACAGATAAT ACATCTTGAG AACAAACAGT TGAGACATCG CTAAATCGG	239

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..224
- (D) OTHER INFORMATION: /standard_name= "DB# 175"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ACATCCCCCG GAATTCATT TCACATAATA GGAAGAGTAT CTTGTAAGG AAATCTCAAA	60
TTGTAAATT GACTGCCTTG CCGGACGTAC TAAGTTTAGC TATAACATCT TTTAGAAACC	120
TGCCATCCA GCAGGTTGGG ACGCTGATTT GCTATCAATA TTCTTTGGTT CACCAAATGC	180
TGAGAATTTT TCGACTCATT GAGAGTGGCC TTTATCTGAG AGCT	224

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..186
- (C) OTHER INFORMATION: /standard_name= "DB# 176"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCCGGCTCG GAATATTAAG TTTAACTAG AAAATTAAAG TCCAAGTGAT TTCAACATCT	60
GATTTCAAAA TTGAAACAA CCACCGAGTC TAAGATGGCA CGAATCTAAG AGAAGCTTGA	120
ACTAGTAGGT GCACCGCCGC CAAAACCTCC AGTCCAGGCC GAATCCAGGT CTTCCACAGA	180
ACCCCT	186

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..253
- (D) OTHER INFORMATION: /standard_name= "DB# 177"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGCGGTGGGT TTGGTGACGA CCAATGGTGG CAGCGAGCTG ATGGACCTCG AAAAAAAGTG	60
ACGGTTTTTG GACGGTGTTT GGTCGGAAAA GGAAAAGGGT CGTTCGGGGT TTCTTTTGA	120
GTGAATCTGG TGGTTGTTAG GTCCTGCTAA GGTACGAGC TCATCGGCTG AACTCTGCTT	180
TTCTGCTTCA CCGGAGAAGA TGAACAATG AGAAAACATT GAATTAGAAC TATGGAGAAG	240
AAAGTCTGGG TGA	253

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..318

(D) OTHER INFORMATION: /standard_name= "DB# 178"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGCCTCTA GATCTGGTGC ACCTGTTAAA AACATAGGTG AGAATCTGCT TATAGCTCGA	60
GCATGGCATT GCTTAAATGT GGATGATGAG GCTAATCGTG GTAGCAGCTG CTGTGAATAG	120
AAGGGCTTTT GATGCCTCTA GATCTGGTGC CACCTGTAA AACATAGGTG AGAATCTGCT	180
TATAGTCGAG CATGGCATTG CTTAAATGTG GATGATATT TGGACAAGTC ACAGAAGGAC	240
CAGGCTCAAC CTACATTTC TCCTGGTGCT CCTCACCAGC CATGATATCC GTCAAGTGTG	300
ATAACCTGGA ATCACCTA	318

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 298 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..298

(D) OTHER INFORMATION: /standard_name= "DB# 179"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGACTACAAA CTTTGTATGC TCTATTCCC TTGTAAGATA CTTATAAGAA CTACAATGTC	60
TTAACAAGGA CAGTTTGTG CAAACTAAAT ATCCTTGATC CATCTGTCAT GAAAGGATCT	120
GAAAAATCCA TTGATTCAGC AAAAATACA CAAAGGACAT ATACTAGCAA TAAAAGTTGC	180
AGGAACACAT ACTGCCGTCA AAAGAGAGTT CAGGCCAGCG ACAATTGTTT TATTAATCCT	240
ACTGGTATCC CTAGAAGTTA ACTGTAGACA ATCCAGAGTC TGACCACATG TTCTCAGA	298

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..233
(D) OTHER INFORMATION: /standard_name= "DB# 181"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAAGTGGCGT TGGAGGATGA GATAGAGGTG GGACAAGTTG ATTGTGGTAC AGATAAGCCA	60
GTTTGAATA AAGCATTACA ACAGCTTTTT GTACATGATA ATCAACATT AATGAACTTC	120
ATTGTCAATC ATAGCAAAGT AACCAATACT GAAATAAGAC AGCTATAGCC AATAGGCCAA	180
GGTGTTCCTC AGTTTCCACT CTTGAATGGA ATGGCTCTTA TGATAACTTG GTG	233

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..258
(D) OTHER INFORMATION: /standard_name= "DB# 182"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CATTGGATTG TTACAGGCTA GAGAACTGT TAGTGCCCTA CCTGGGATGT TCCCTGGTAG	60
CTTGATGCCT GTACTTCTTC AAGCTGCTGT ACATGTGAGA GAGAACAAGG CTGCTAAAGC	120
TGAAGAAATA TTGGACAGTA TGAGATAAG TTTCTGACA GGTCCAAGGT TATCCTGCTT	180
GCAAGGGCTC AGGTTGCTGC AGCTGCTGGC CATCCGAGAT TGCAGCTGAT TCCTTGGCGA	240
AAATACCTAG ATTCAACA	258

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: /standard_name= "DB# 183"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGGGGTGGG AGGAAGCAGA CTTCCGGAAG GAGGGGGAAA GAACTCTTAC ACTATCTTGG	60
TTTCCCTGT ACCAATCCTC TCTTTTCGC CCATCAAAGT TTGGCGTATA TTCAGTCTTA	120
ACATCCTCAA TTTGTCTACT TCTTGAGTGT TTGTCAGTTC CGGTGTTTGA TTGTATTCCA	180
AAGTTCTAAG TTACCTTGGC TTAAGTGCAA ACTTTAGTTT CTGTAGTAGT TACTATTGT	240
TTGTGATTGT CTAGACATTC TTTCTCGAGG CATATTTGTT GGTGATAAGC AGGTGTGCCA	300
CA	302

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..288
- (D) OTHER INFORMATION: /standard_name= "DB# 187"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ACCAGAAATG CAGATTGATA GAGATGATTC CACAAAGGGA ATCTTAATTG AAACAAGAAG	60
ATATCCTGTG AATATATTTA CAGATTGAGA TAAGACTTCT ATAAAACCTC AAAATTCCTC	120
AATCATCTGA CACCTAGCTT ACTATTTTAC CTGGCTTCTG TCAGCCTATT TATACCAACA	180
AGACCTACAT CTTAAGAAAT TAGAGACAGA TCCTAATAAT TCATCTCACT ACATGTTATT	240
GACATTGCCG CATCTCGTGA TTTTATCCAA AGCAGCAACC TTAGCTCG	288

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..245
(D) OTHER INFORMATION: /standard_name= "DB# 197"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGATGGAATC AAAAAACAT AATTACTGA AACCATCCCA AAAATTGGCA TAGGTATAAT	60
AAATATATTG AGGTTAAAT TGTCAAAATT TGAAGCGCTA ACGACTAACA AATGAAGATT	120
CAGTATCGTA GTAGAGGGTT GCTGTGAGGC GAGGGAGGAG ATCCTTGTGT GAGTGAGATT	180
TGCTTGAATC GATGGACAAT AAAAATCAT ACAGCTCTTA TAGATCATTC ATGTCACCTA	240
CCTAA	245

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..153
(D) OTHER INFORMATION: /standard_name= "DB# 198"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAGGAAAGTT TATGCCCCTA TGGAGCTTTT CGACTGCAGA AACTCACTCA AATTAGTAAT	60
TGAAAATGCA TAGCAAGACA ATATCTCACA GGCCACATAT AGGCCATAAT ACATGTAGTA	120
TGTCTTATTT AAAGAGACGA ACATTAGAAC ACT	153

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

71

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..239
(D) OTHER INFORMATION: /standard_name= "DB# 199"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AGTGTGGAG AATCAATCTG TAGAATACCG CTTACGGATT TCCATTAGAT TTGACCCAGT	60
TAATGGTAGA GGAACGAGGC TTGGTTGTTG ATGTTGATGG TTTTAATGTT GCTATGGATG	120
CTGCCAGGGA AAGATCAAGA AATGCTCAGA GCAAGAATGC CAGTGGTGCT ATTGCCATGG	180
ATGCTGACGC ATCTGCAGCA TTGCACAAGA AGTATCATTT GTTGACGCGA CCCTTCTTG	239

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..278
(D) OTHER INFORMATION: /standard_name= "DB# 201"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CGTCAATCGT TAATTGGATT CAATATGAGT GGCTGGGTTG CTTACATCCA ATCTTTGACT	60
GACAGCTGCA ATGTTATCTC CAGAGCGGCT ATTGTTGGAC TTAATGATGG AGGTAGTGTT	120
TGGGCTCGAA CGGAAGGCGA CAAAGAATTA AGGCTACCGT GTCGGAATC AAGAAGTTTG	180
TTGAACCTTT TGACAATCTT GATAGTGTTT CAGGAATGTC CGCAGATCTA GAAGGTGTTT	240
ACTACATTGT ACCGAGAACT GAGGAGAACC TCATTTTT	278

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..261
(D) OTHER INFORMATION: /standard_name= "DB# 203"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAAGCCAGAA ATCGATGTTT GATACATGTC TGGCATTGTC ACAGGTGAAT GGGAACTAAT	60
ATGACTTTAC ATCAACAAGA AAAATGTAAA CGCAGCAGGA GCAGTTACAG CTTTGCTAGA	120

72

AGAAGAAGCA TTTTCTCTAA TAGAAACAGT AAATATTAGC AAATAGAAGG CAAAGGTGCA 180
GAATGTTTAC AGCATTACAG TTGAGCTAAA TTCGAAATAC AGGTTTGATT CTTCTATGCC 240
CCGTCTGACT GACAAAGTTG G 261

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: /standard_name= "DB# 205"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AAACGTTTTA AAAAGTTTGG GAATTAAGTT TTCAACAGCA ATTTCACTAC ATTAATCTGG 60
TCAAAGTAAT ACATTAATAA CTTATTAATA CTCTCCTAAA ATTCTCATAC TGAACAACTA 120
CATATTCCTC ATAAGTCATA TATTTTCATC CTCTTCAGT TAGTTTCTT CTTACGCA 178

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..244
- (D) OTHER INFORMATION: /standard_name= "DB# 207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AATCTAAGCT CCAAGAACTA GTCCATAGTT TTTTTTCTG TGTGCCCTAA AGACCATAAC	60
TTAGAGCCCA AATCTTTTTC TACATCAGCA AAACAACGAT TTGGTGTACC AAACGTGTTG	120
GAACTCGGAC CATTGATGCT AATCATTCCA AGCTGGTGTG GAATTTACGC ATTGGCTGCT	180
GGTTGTAATG GCTCTTCTCT TTCTTCTTGC TGCAGCAAGC CTGGCACTCC CTGCAGCAGC	240
CTCT	244

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: /standard_name= "DB# 208"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATTTCAGGT AGGTAATCCA ATACAAAGCT AATATTTGAA GGAAGTGTGT TTGCAGTTAA	60
AGACAACCTAC AAATAAATGT TCATGTTTAT GGATGGGTTT GGGTAGAGTA TTTTTCAGAA	120
ATAGCAGAGG CGAGAGTGTT GCTATTGTTA AGCCACAGAT GAAGAACCAT TTGGGCCAAA	180
CAATCCTAAA GGATTGTGG GCAAGCTCTT GGGCAGCCAG GCTTAAACGA TCAGTCAGAG	240
TTGGGAAACA GGGTAAGCGG CCGCATGACA TGCTTGAG	278

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: /standard_name= "DB# 209"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AAGGAAAGTT TATGCCCTTA TGGGAGCTTT TCGACTGCAG AAACCTACTC AAATTAGTAA	60
TTGAAATGC ATAGCAAGAC AATATCTCAC AGGCCACATA TAGGCCATAA TAACATGTAG	120
TATGTCTTAT TTAAAGAGAC GAACATTAGA AACT	155

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 312 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..312
(D) OTHER INFORMATION: /standard_name= "DB# 210"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AGCAGAGCCG AATTAAGAAT TAGAAGATGA AAGCATATGC AATTGCACTC ATTGTCTGTG	60
GATCTGTTGC AGCAGCTCTA GTTTTAATAT CGTGTGTGTT TTACAAAATT GGCCGAAAGA	120
AAAAGAGTTC CCCAGTGACT CGGTATGTGA CCAGTGGTTC TCCGGTTATT CCTCTGCCGC	180
CGAAGCCTTT ACCAGCAAAT CGTGATGTTG AAAGGGCGAA ATTAAACCAA GACAATACAG	240
CAATGAGAGA TGGTGGAATG GTAATTCTAG GTGCGGCTGC TGCTGCAACA GTTGTACGCG	300
GTGTTATCGA CA	312

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'
- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..186
(D) OTHER INFORMATION: /standard_name= "DB# 212"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCCCGGCTCG GAATATTAAG TTTTAAGTAG AAAATTAAAG TCCAAGTGAT TTCAACATCT	60
GATTTCAAAA TTTGAACAA CCACCAAGTC TAAGATGGCA CGAATCTAAG AGAAGCTTGA	120
ACTAGTAGGT GCACCGCCGC CAAAACCTCC AGATCCAGGC CGAATCCAGG TCTTCCACAG	180
AACCCCT	186

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large

Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..189
(D) OTHER INFORMATION: /standard_name= "DB# 214"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
GCAGTCACAG GAATATATAC TTGAGACTGG GTCTGCAAGG AAATGTTATT GCCCGAACTG    60
ATAGGACGGA TGCTTGTTAT GGGCAATGAA CTTCTGAAC CATTGACACC ATTTGAACAG    120
TCTTCTTCGG TGGACTCACC GGACTTAGAT GTCGGAGAAT GTGACGCTTC AGATCCCATG    180
TAAACCTA                                     189
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..290
(D) OTHER INFORMATION: /standard_name= "DB# 215"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
CTGGAGAACA GTTTAATGAA TATTTTCATT TAGCTCTCAC GTTCATTCTC ATTTACCGAA    60
GCAAAGAGAA TTTTATCAAA ATGGTTCAC TACATGTAA AGAAACACGC CTATACAAGT    120
GTAAAATTGT TGCTGAACAT GTGAAAACAT ATGTACAAAA CCTATCCTGC ATTCCATGTG    180
GTGCTGTCCG CACCATGGGC ACAACAGAAA CAGTCTACAC GGAGTGCGGC ATAGAGAGGG    240
AGAGCGCATA TGGTCGGGTG AGAGGACCAG CCACACGACT GAGCAGCCTG    290
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..238
- (D) OTHER INFORMATION: /standard_name= "DB# 216"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AGAGTAAAGG CAAAGGGTTG TTATTCTGTA AGGTATTCAC TAAATCTCAG TTACTGCAGT	60
ATAAATAGAT GATGGAGGAA ACGTCTAG CTACATAATT GATCCCTCC CTATTCTCAT	120
TTCTTGTTCA ATGTATTACC AATGTCTAGC ACAAACGAT ATTTACGTC CGATTTCAAA	180
AGACGTTCCA ACGCGGTGTT AACGTACTCA TTGGCACCAT TCAATATCTG GTGTTATG	238

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..260
- (D) OTHER INFORMATION: /standard_name= "DB# 217"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AAGAGGCTAC AAAATACATC AAACCTTATA GTAAAACATT CTAGAAGTC CAAAAATCAC	60
TAGTAAATTC CTGGGATAAC TCTGTAAGGA ACCTTTTCAC AATACAATTT CCAGTACTTG	120
CCATACCTTG CCTTGCATCG GTCATCGTCC CTTTACGTC GATCGAGAAG GAGGATTATT	180
AGAAAGATGA CGTAGAAGTA GGAATGAGT GGTGAAAAG AGCTGGTACA CTCAGAAAAT	240
GCCGTAATAT TTCTGGACTA	260

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..124
(D) OTHER INFORMATION: /standard_name= "DB# 218"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGACCCCAA CAGAGAATTT AGTTGTTATT TGAGGTTGAA ACGAAAGCTA AACGCATTCT	60
TAGCAACTAC CACTTCCTCC CCCTAAAATA AAATAAAACC CAGCATTTTC GAGGTGGTCC	120
TAAC	124

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
(B) LOCATION: 1..263
(D) OTHER INFORMATION: /standard_name= "DB# 220"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAGATGGTGT TTGCTAAGGG AGACCCCGGC ATTGCTGCTT TATACGACAA GCTTCTGGTT	60
TCTGAAGATT TGTGGTCCTT CGGTGAGCTT TTGAGGTCTG ACTATGAGGA GACAAAGAGC	120
CTCCTGCTTA AGGTTGCTGG ACACAAGGAA CTTCTGGAGA ACGATCCCTC CTTAAAACAA	180
CGATTCAGGC TGGTGATTC CTATATCACT ACTTTAATGT CTGCCAAGCT TACACATAAA	240
GAGGATTCGT GATCCAATA CAA	263

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..253
(D) OTHER INFORMATION: /standard_name= "DB# 221"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ACCGTGAGGG GGATTTT TAG GGGCCTAATT TTGTTGGGAC TCTGTCCTT GCTACTGGTC	60
GCGCCTTGGT AATATGTAA AATGGCAGAC GAAGTTTAGG TTGAACAATG AGGAAGCAAC	120
TTTAAACATT TGAGTCCCA TTAAGCAGAG TGGTGAGCTG CAAATGGTAT CTGCTATATC	180
CTATGGGGTT TAGAGTAGAC CAAGGTACAA ATATAGAGCG CCTTGATATT GAGGCACTAA	240
TGTGTATTGA AGT	253

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..196
(D) OTHER INFORMATION: /standard_name= "DB# 222"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GGGGGGCCTC TTTTGTAAC TTATCTGTGA GCAGTGACCA ACGTCTCTAT AAACCTCAAT	60
CCATCAAATC TGGCGCAAA TTTATCTGTA GATGTTGATG CTTTCACCGA TTTTGAACAA	120
TCTTCACCAG TTTTCTTCAA ATTATCGTCC TTGTGAAGAG AAATTCGAAC TTTGGATACA	180
GAAGAGACGG TGACCG	196

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..148
 - (D) OTHER INFORMATION: /standard_name= "DB# 223"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATCCCACTTA GGCTGATAAA GAAATATTAG GGGTAGAGAA TATTCAGTA TTAATTAAAT	60
TGACTCTACC AATAAGCTTA AGAAAGTCGC TAATTATGAC TGCTCAAAGT TCCTAAGACA	120
AGTCCAGGTG AAGGATTCTT TATGCAAG	148

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..99
 - (D) OTHER INFORMATION: /standard_name= "DB# 224"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAGTTATGAA CTTACTTTAT GATATTCAAA TACGAACAAG CTAATAATAT GTTTAGCTTT	60
ATTTTCAGGA CATAAGAGTC ATACATCGTT CAGCGCTTG	99

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1..226
 - (D) OTHER INFORMATION: /standard_name= "DB# 226"

80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGAAAGAAA AAAAGAGGTG AAGAAATTGT AAGAAAAACT GTTGTACAA GGAAATGTCA	60
CTTCACCATT AAAATTTTGG AAAAAACATG GACACAATCC CTTTCAATGG GTGGTGCTTC	120
AAGATATAAC ATAACGAAGT TAAAGAAATA GATGAGAGGG GGGAAAGACA ACACAAGACA	180
ATGTTTTCCC CCTTTATATT AAAAGACATG TTTTTTGT TATGT	226

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..276
- (D) OTHER INFORMATION: /standard_name= "DB# 227"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CACATGCTGG CAAGGGTATA TTAGCAGTC CATCACTGAT GGTCTGGAT GCTTGATGT	60
GCGCTGCTCT GCTCCAGGGT GTGATTATGC AGTTGACTAT ATTGTTGGA GTGAAGCTA	120
TGATGTTACT TGTGGTGCT CATATAGTTT CTGCTGGAAT TGTACCGAGG AACTCATCGC	180
CCAGTTGATT GTGGAAGTGT GTCTAGTGA TTTGAAGAAC AGTGCAGAGT CTGAGAACAT	240
GAAGTATAT TAGCTAATTC TAAGCCTTGT CCGAAT	276

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..245
- (D) OTHER INFORMATION: /standard_name= "DB# 228"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGTGCAGTTA CTCTATCTTT GCTATAGCCT GGTGTGCATA AAGTTGTGGT GCATACAAA	60
GTTTGGATAG TTTCCAAGA TGTGAAGATG ATTAAGTATT TTATCACTTT GTAGGAGTGG	120
AAAAGGGCTC GAAGGACCCA CAGAGGGAGA AAGTGGGAA AATAACTATT GATCAATTGA	180
AGGTAATTGC TCAAGAGAAG TTGCCGGATC TTAATTGTTT TACTATTGAA TCTGCAATGA	240
GGATA	245

81

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..233
- (D) OTHER INFORMATION: /standard_name= "DB# 230"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AAGCCAAGTT TCTATGACCA GAAGCAGTCA CATACAAGTC CATGCTCAGT AATTATAGAA	60
GCAGTCACAT ACAAGTCCAT GTCAGTAAT TATAACTGTT TCGCCACATC AAAATTCAAT	120
ATCTATCATA TAGAGCTGTG CCAAAGGCAA ATAAACATAA CTGTTTTTGC CCAAGCTAAA	180
TCTAACGTAA CGACTTTCAA TTGCCTCGTA TTGGGATCTG CCATCACATA ATG	233

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: /standard_name= "DB# 231"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CGGGACCACA GAAACACAAC ACACACCGGA TACAGAGAAA CAAGGACCGG CATTGTCTTC	60
TGTAGGACAG ACACAACGAC TTCAACCAAG TTCCACAGAA ACTAGGACCC GGA CTCAAAC	120
AAAACCTTCA CCGTAAAGTT CCACACGTTA AACAACAATA TCCACCTAA GAGT	174

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

82

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: /standard_name= "DB# 232"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

AAGAGAACGA AACGCACGTA ATGGTTATCA TAGCTTTCCA CAATTTACA TTAACCAAAA      60
CAATTGCACT ACTTGTAGGC TAATGAACTG GTGATGGTTG AGAAACTGGA GATGTTTATT      120
AGTGAAGGAA AAACACAGAA CAGGTTTAAA CACACTGGAA ACATAAATAA CAGAAGACTG      180
CTGCAGAAGT CACACTGAAC TCATACCAA GACCATTTCA ACTGCTACAT TAGACTAGAA      240
GAGACCTTCC ATGACTGCCA CAGCTTCCTC TCAGCATACC TCTGCTC                    287

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..277
- (D) OTHER INFORMATION: /standard_name= "DB# 233"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

ACCCATCAAA AAGTGATTTT ATACTCTCAG TGCACATATG TTCAGCACTC GTGCTGTCTG      60
ATCTAGGGCC AAAACTGCGC ACAGGTCACA ACCTGCAATC ACCTCATTAC ACATTTGAGA      120
AATGAGCAAA ATAATACTTC CACATTGAGC ATAAAACAAA AGTTCATCTG ACGTTGAATC      180
TGTTTAAGAA TGAGATGATG AATCTGTTTT CTCAGCCAAA TAGTGCTCAA GCATATCTCT      240
CATCATCATC TCACTCATCA CTCGAATCAT ATCATCC                                277

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..255
- (D) OTHER INFORMATION: /standard_name= "DB# 234"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGCCCTCA ACTAAGTTGG CCAATTTATT GGATCATTTT AATTAACAA TAACTGAAAT	60
ATCAGAGAGA CAACGTTTCT CATATCTGCA AGAAGCTAAA AAGGCGGCAA CGTCGGTGCC	120
CTTACATGTA TGTGCTGCAC GACCTTAAAA AGTCAAAATT TGAAGAAGA TGATCTTCCT	180
ACATATTAC ACTGTTTGTG GCAAAGAAC ACCGCAAAAG AAAAATCCTG TCTCATCATC	240
GACAAGCAGG TGCCA	255

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..202
- (D) OTHER INFORMATION: /standard_name= "DB# 236"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAGAAGGGGG AAAGGGGGAG CTCGGAGGGA GGGTGAGGAA ATGTTTACAC CCTCTCCCCC	60
GCATGCTGAG GTCCTCCAC CAACTTAAGG AAGCAAAATT ACTACAGCAA ATTTCTGAAA	120
TTTAGCAAAG AGGAACAAAA CAATTGCAAC CACTGATTTC CTGCTTGCTC GCTTGGCCGG	180
GTGTGCGTCG CCGTGTTGGG CT	202

84

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..77
(D) OTHER INFORMATION: /standard_name= "DB# 239"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGTGAAGCG GCGGCGCGG CAGAGGAGG ATGATTATT TGGTGT TAG AGGGCATGGA 60
GGTCACTG TAGCGAA 77

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 1..222
(D) OTHER INFORMATION: /standard_name= "DB# 240"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAAGCAACAC AACCTCTTC ATTCATCTG GCAAAAAAGT ACAATCAATC ACTCAAAATT 60
GACTTATAAC TCATAACAGT AGGAATCCTA AATAGATGGG AAATTAACAG AAGCATTATT 120
CAATGAAC TG ACAAAGACAA TATGTCATCA TGTAAGGTCT AATGAACCAA AAATGCAATG 180
CTGATATGGA AATGAAATTA GTAGATTGAG ATCTTCTCGC AG 222

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 309 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..309

(D) OTHER INFORMATION: /standard_name= "DB# 241"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CCAAGATACT GATTACTGTT TTCTGTTGAA CCGGCATGTC TGTATCTTGT GTATATAGTT	60
TAATTCTGGA GCATGATGGC TAAATGAGA TCTTGATAAC TAGGCATAGT AATTGATAAA	120
TGTGTGCTTT TAAGCATGAT ATAGAGGTAC ACCACAGCAT TACCCTAAGT CTAATAATTCA	180
AAC TAGGTGT CTAATAATCT GGTAGAGTGA TGAGAGTTCA AGTGAGTGTG AGGAAGATTT	240
GAATAGTCCA TATTTGACT GAGCTAGAAC TTGGCTGATC CTGAGCCTGT ATTACGCTAA	300
GAAGTCCTA	309

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..246

(D) OTHER INFORMATION: /standard_name= "DB# 244"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGAAGTGCTG GAGGCCCTTC TTCTGCAACA ATAGTCTTCA CACAATCAAC AATGCTCTTG	60
TATTGATTGG CAGAACCTG AGTCATTAAT CTCGTCTTAA TGACATCAAG AGGAGTAGTT	120
ATAGCTCCAG TTAGAGCACC AGCAAAAGCA CCGATAACTG CATTCTCTGG ATCATTCAAT	180
TCCCTTTTGG CAGCCAGCTT ATACCTATC CGCAGCTGCT CATAGTAACG ACTGGATGGC	240
ATCAAC	246

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

86

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..205
(D) OTHER INFORMATION: /standard_name= "DB# 246"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GCGGAGGAGA ACATCTCCGT GTTGCTGAAG TTGCGCTTC AGGTCGTCTA TTTTCGACGT	60
TGGTGGTTGG ATCACGCGTC CGTCGGAGCT CGGAGGTTTC ACCTGAGACG ACGTCGCCGC	120
AGCTGGCTTT GCGGTTGTTT CTCCAGGAGT TCACTGGGAC TGTGTGTTG CTCACCGAGA	180
GCTCGTGCTT TGTGTGTTT GTTGC	205

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..107
(D) OTHER INFORMATION: /standard_name= "DB# 247"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GGCGGCGTTG TGAAGCCTTA TCATGCTTAT ACGCCATCTG GGTAGCGTAT GGTGAGCCTT	60
TTTTTTGAAG TTATGGGAAG GAAAAGGACT ATATCCCTT TGGTCGA	107

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..209
(D) OTHER INFORMATION: /standard_name= "DB# 249"

87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

AGACCCACAA ATCAAACTCA AACAAATTCA ATTTAGAACT CATTGGATAA AGGAGCATGT	60
TCTGTGTCA TGAACACATT TGTGTAAATA AGACCAGCCA AACTACCACC AACTAATGGA	120
CCAATCCAGT AGATCCAGAA ACCCTCAAAG TTACCACTAA CCATTGCAGG TCCAAATGAA	180
CGAGCTGGGT TCATTGATCC ACCGGAGAA	209

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..199
- (D) OTHER INFORMATION: /standard_name= "DB# 250"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTCACATATC AATGATTTTC TAGCGGACGG CAAAATCCTT ACAAGTCTAG AAACCTCAATG	60
ATGTGTAAG GCTCAATCCA TGCGAGCAGA ATAAACCCT AGATACCATA GAGGGAGAGG	120
AGGAAAACGG AGAAAGCAGT GGTGGGACGA AGCTTACTGG ATTGGAATGT GTGTAGGTGG	180
AGTGATGGAT GGACCTGAA	199

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc feature
- (B) LOCATION: 1..211
- (D) OTHER INFORMATION: /standard_name= "DB# 252"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATTAATAAAA TCTCCATTCA TTTCATTCA AGAGAACTTT GTAAACAAGG ATCCACAGGG	60
TAACATCAGG GTAACAATAG AGGTCAAAAG CAGAACTA ACAGTAACCA GGGCAAAACC	120
ATAAACGTAA CTTTCATCAAC ACTTCGAAAC CATAAGTAAG TTCAGACGAG ACCAATCTAA	180
AAAGCCAACA GAAATCTAA TCCTTATCGG C	211

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs

88

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(fi) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..203

(D) OTHER INFORMATION: /standard_name= "DB# 255"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TGAATATGAT GGCCTCGTA AGATTTAATA TGAATTGAGC CTTTGGAGTT TGAATATGAA	60
TGATGATCTT GGGGATTGA ATATGAATGG CCCTTTGGCG TCTTGAATGG CAATGGCCTT	120
TTGGCATTG AATATGATGA CCTTGGCAGC TTGATATATG CTTTGGCATT TATATGATGC	180
TTTGGCAGTT TGAGTAGCGG CCG	203

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1..184

(D) OTHER INFORMATION: /standard_name= "DB# 256"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCTATCACT CAGATTGCTA AAAAAAAAAAC ACTTCCATTT GCAGCATCTG ATTACCACAA	60
TTTTCTCTGG TAATTCAAAA AAAAAAACC ATACTATTAC ATTAAAGGAC GAACCTTTTA	120
GTTGAAATAA TTGTCACCAC GAATATGAAA CTGGACTTCT AACTTGGTTT TGAGCATTGT	180
TACC	184

89

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..188
- (D) OTHER INFORMATION: /standard_name= "DB# 263"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGGGTCGCAT GTTGGAAGG AGCCACAGAA GTTTATTGAT GAGGTCAATA AAATATTTGG	60
TATGATGTCA ATAACGCGT CGTTATAGGT GAGATTGGCA TCCTCCAAAC TCAAGGATCG	120
TGACGCACAT AGGTTTACTC AGTGGAAGA CACAACATGA TTTTGGAGAA CTCAGTAAGC	180
GGCCGCAT	188

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: /standard_name= "DB# 264"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTTGAGGATC TGAATCAACC TCGTCAAATG CTCGTGGAGA TGCTTTGTGA AGAACGCGGT	60
CTATTTCTGG AAATAGCTGA CATAATAATA GGATTGGGCT TGACCATCTT AAAAGGGGTT	120
ATGGAACGCA GGAACGACAA AATATGGGCG AAATTCGCTT AGAGGCAAAT AGAGACTACG	180
AGATGAATAT TCA	193

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..218
- (D) OTHER INFORMATION: /standard_name= "DB# 265"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGATGCTGAT CTTGGTGGG ATGTTGACTC GAGCAAGAGT ACGTCCGGT ACATTTACAC	60
CATAGGTGGA AAAGCAGTAA GTTGGATGTC CGTGTCTTTA GAAGTATGTT TCTCTTTCAT	120
CCACTAAAGC TGAGTTTGTG GCAATAGCTG AAGCTGGGAA AGAGATGATA TGGATGGCAG	180
ATTATCTTGA GGAATTGGGC AAGAAGCAAA GCAGAATT	218

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: /standard_name= "DB# 266"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGCAAACAAA GTAGAATTAC ATTGCAGTTT CTCCCTTACT AGTCATCAAA TAAATATTCA	60
CAAATTGAAA CACAGCTGTT CCCTTAACAA CCCTATGAAG GGAGATTAAG AAGTAACTAA	120
GTTGCTTTCA CGGAACCTTT ATTCATTGCA CCCCAGCAC ATAGACATTG CTGTTACAGT	180
CCAGCTGCTC CGG	193

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: /standard_name= "DB# 275"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAGATCATCA ATGACCGGGA AACTGGTAGA TCTAGAGGAT CTTGATGGTC GCAACATCAC	60
CGTGAACGGA GCTCAATCAC GCGGAGGGGC TGGAGGTGGA GGTGGAAGAG GCGGGGGTGG	120
TTAGGAGGTG C	131

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..220
- (D) OTHER INFORMATION: /standard_name= "DB# 277"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCAGTGGGCA CATTGTTAGG AGCAATGACA GGAGCTTTGA TAGGTCAAGA AACTAAAGTG	60
GATTCAATAG AGGTGCCCGG GTTGGAGCCA TTTCTGGTGC TGTTTCTCT CTTGAGGTCT	120
TTGAGTCATC TCTGATACTA TGGCACTCTG ATGAATCCGG AGTTGGATGT GTTCTGTACT	180
GATTGATGTA ATAGCTAGCT TGTTAAGTGG TAGACTAGTT	220

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..323
- (D) OTHER INFORMATION: /standard_name= "DB# 279"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AACTAAGAAT GCTTAGATGC TGAATAACC TTGCATGTTG AAGCAACACA AAAACTGAAT	60
AAAATTTTGA CAATGTCCTA ATATCACAAG GACACGAATA GGCAAGTGAA CATACCCATA	120
TCTCTAATGC AGAGCCCTAC TGATCCAAAT ATGAACATGG ACTACATGGT'TAAAAATTTT	180
ACACTCAGAT GAATTAAGCA AGTTGGCACA GAAGAGGTTT TGGTGCCCAA CAGAAGAGTG	240
GATCTCACCA AGAGCCGCCT CTACCAAGGT TTGAGGTCAC CAACTGGCCA GCAGTCCAGT	300
TTAAGGCTCT CCCC GGCTTC AGT	323

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..336
- (D) OTHER INFORMATION: /standard_name= "DB# 280"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATCTAACAGT TGAAGGAGCA GAAGAATTAG AAAGCCACGG AGGAAGAAGA GTTTGTGGCG	60
TAGGAGTTGA GGCATCGGCG TGGAGGAAAC CTCCATTAGA AGTAGCCATA GGTAAACCTG	120
GGACACTCCT TTCTTTCACA ATCTTTTCTG CAAAGGTTTC GAGAACGTGA TCGTATTTTC	180
CATCGTCTAC TGGATCACAC CTTGTTGTTT TCTTCTGCT CTCTCTGTTG CTTTCTCTTT	240
GAAACTTCCC ACCACTTTCC TAATCTTTTA GCAGTTCGAC CTGGTACTTC AGCTGCTATT	300
TTTCTCCATT TGTTACCGTG TTTGGCTTGT AGTTGA	336

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..278
- (D) OTHER INFORMATION: /standard_name= "DB# 288"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ACTTGAGAAA TACTTTGT	60
TTT AGTCTAAAC AGGAAAAGT ACAATTTGCC TTCTGGAGAA	
GAATAAGATC TTTGTCTCAA CTCACAAGCT AATAATACTA AACAAAGCAA TGAAAGGGTA	120
GAAACCTAG CTAAGAGCT TCAGGAAAC AGATAATACA TGCCAAACGG CAATAATATA	180
GTATTCCAAG TTGCGCATCA CCCATAGCAA CACCATGACT TCCATTACAC ATGACTGGAA	240
ACTTATTGGT AACCAAAATT ATGGGTATCA GCGCAGCC	278

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: /standard_name= "DB# 289"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TACTCACTAG GAGCACAAGG TTGAAGTTCT ATTTATAACA AAAATATGGA ATAAAACAGG	60
AAAGCAAAAC TTCAAAATTC AAAACACAAG GCACTTCCAT TAAAGTGCTT TCATGAAATT	120
CTAAATTCTC CTCAAAATTC TAAACAGGAA AACTAATTTA GACTGATCCG ATTTT	175

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Lycopersicon esculentum* cv 'Rutgers Large Red'

94

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..112
(D) OTHER INFORMATION: /standard_name= "DB# 291"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTGAATTCT AGAGCGTTGT GAGCAAGATG ATGGATTCT TGAAGTTTT ATGAGGAAGA 60
GTAGATGGAA TGACGGGCAT GCTTCCAAGT CAGCAAAGGA CGATGGGAAA GA 112

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 825 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lycopersicon esculentum cv 'Rutgers Large Red'

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..825
(D) OTHER INFORMATION: /standard_name= "DB# L23762"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTCTTCTCC ATTCTTTCA AAATTAAGT ATTGTTACTC TGCTATTGGC TCAAAACCTC 60
TGCAATCTCC GTCTCCTCA ATTTCAACTC AAGCAAATCC ACCTCTTTCA CTAGTTTCAT 120
CACTTTCAGA TCAGGGTTTG GAGTTGAAGG TACGGGGGGC TAATTGATGG CGTCCAAGAG 180
GATATTGAAG GAGCTCAAGG ATCTGCAGAA GGATCCCCC ACATCATGCA GTGCTGGTCC 240
AGTGGCAGAG GATATGTTCC ATTGGCAAGC AACAATCATG GGGCCTACCG ATAGCCCTTA 300
TGCTGGAGGT GTATTTTGG TTTCAATTCA TTCCCTCCA GATTATCCTT TTAAGCCTCC 360
AAAGGTTGCC TTCAGAACTA AGGTTTCCA TCCCAACATC AACAGCAATG GAAGTATTG 420
TCTGGATATT CTTAAGGAGC AGTGGAGTCC AGCATTAAAC ATATCCAAGG TCCTGCTGTC 480
CATCTGCTCT CTGTTGACAG ACCCAAACCC AGATGATCCT CTTGTACCTG AAATTGCTCA 540
CATGTACAAG ACTGACAGGG CCAATACGA AACCCTGCTC CGTAGCTGGA CTCAGAAATA 600
TGCAATGGGA TGATGCCCAA AATGTCTCCA GGCATGTCTG GGACTTTGTA ACAGCAATGT 660
CTTATGTGCT TGGGGTGAAT GAATAAATC CGTGAAAGAA CTTAGTTACT TCTTAATCTC 720
CCTTCATGAG GGTGTGTAAG GGAACAGCTG TTTTCAATTT GTGAATATTT ATTTGATGAC 780
TAGTAAGGGA GAAACTGCAA TGTAATTCTA CTTTGTGTTGC CAGTT 825

95

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligo)

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..26
(D) OTHER INFORMATION: /standard_name= "P35"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTAAGCGGCC GCAGCGTCAG TAACTC

26

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (oligo)

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..22
(D) OTHER INFORMATION: /standard_name= "P36"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TACTGACGCT GCGGCCGCTT AC

22

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..35
(D) OTHER INFORMATION: /standard_name= "P39"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ACTCTTGGGC CGAGTTGGCC TTTTTTTTTT TTTT

35

96

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /standard_name= "P40"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

ACTCTTGGGC CGAGTTGCC TTTT

24

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (primer)

- (ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..18
(D) OTHER INFORMATION: /standard_name= "P46"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GGCCAAGTTG GCCTTTT

18

WHAT IS CLAIMED IS:

1. An isolated polynucleotide capable of hybridizing under stringent conditions to a nucleic acid having a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 18, SEQ. ID. No. 20 through SEQ. ID. No. 33. SEQ. ID. No. 35 through SEQ. ID. No. 45, and SEQ. ID. No. 47 through SEQ. ID. No. 109.
2. A composition comprising an isolated expression cassette having a nematode-responsive promoter operably linked to a polynucleotide encoding a polypeptide that inhibits nematode infection, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.
3. The composition of claim 2, wherein the polypeptide inhibits signal transduction associated with feeding cell formation.
4. The composition of claim 2, wherein the polypeptide is an antibody.
5. The composition of claim 2, wherein the polypeptide elicits a defense response against plant pathogens.
6. The composition of claim 2, wherein the polypeptide is toxic to plant cells.
7. The composition of claim 2, wherein the polypeptide is toxic to nematodes.
8. The composition of claim 2, wherein the nematode infection is caused by root knot nematodes.

9. A composition comprising an isolated expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a
5 plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID No 1 through SEQ ID No. 109.

10. The composition of claim 9, wherein the
10 polynucleotide is linked to the promoter in an antisense orientation.

11. The composition of claim 10, wherein the polynucleotide is selected from the group consisting of
15 SEQ. ID. No. 1 through SEQ. ID. No. 109.

12. The composition of claim 9, wherein the polynucleotide transcribes a ribozyme.

20 13. A nematode-resistant transgenic plant comprising an expression cassette having an isolated nematode responsive promoter operably linked to a polynucleotide encoding a polypeptide which inhibits nematode infection.

25

14. The transgenic plant of claim 13, wherein the polypeptide inhibits signal transduction associated with feeding cell formation.

30 15. The transgenic plant of claim 13, wherein the polypeptide is an antibody.

16. The transgenic plant of claim 13, wherein the polypeptide elicits a defense response against plant
35 pathogens.

17. The transgenic plant of claim 13, wherein the plant is a tomato plant.

18. The transgenic plant of claim 13, wherein the polypeptide is toxic to plants.

19. The transgenic plant of claim 13, wherein the polypeptide is toxic to nematodes.

20. The composition of claim 13, wherein the nematode infection is caused by root knot nematodes.

21. A nematode-resistant transgenic plant comprising an isolated expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID No 1 through SEQ ID No. 109.

22. The composition of claim 21, wherein the polynucleotide is linked to the promoter in an antisense orientation.

23. The composition of claim 22, wherein the polynucleotide transcribes a ribozyme.

24. The transgenic plant of claim 21, wherein the polynucleotide transcribes a ribozyme.

25. The transgenic plant of claim 21, which is a tomato plant.

26. A method of conferring nematode resistance on a plant, the method comprising introducing into the plant an expression cassette having a nematode-responsive promoter operably linked to a polynucleotide encoding a polypeptide that inhibits nematode infection, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

10

27. The method of claim 26, wherein the expression cassette is introduced into the plant using *Agrobacterium*.

28. The method of claim 26, wherein the plant is a tomato plant.

29. A method of conferring nematode-resistance on a plant, the method comprising introducing into the plant an expression cassette having a nematode-responsive promoter operably linked to polynucleotide which inhibits expression of a nematode-induced gene, wherein the promoter is from a plant gene which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ. ID. No. 1 through SEQ. ID. No. 109.

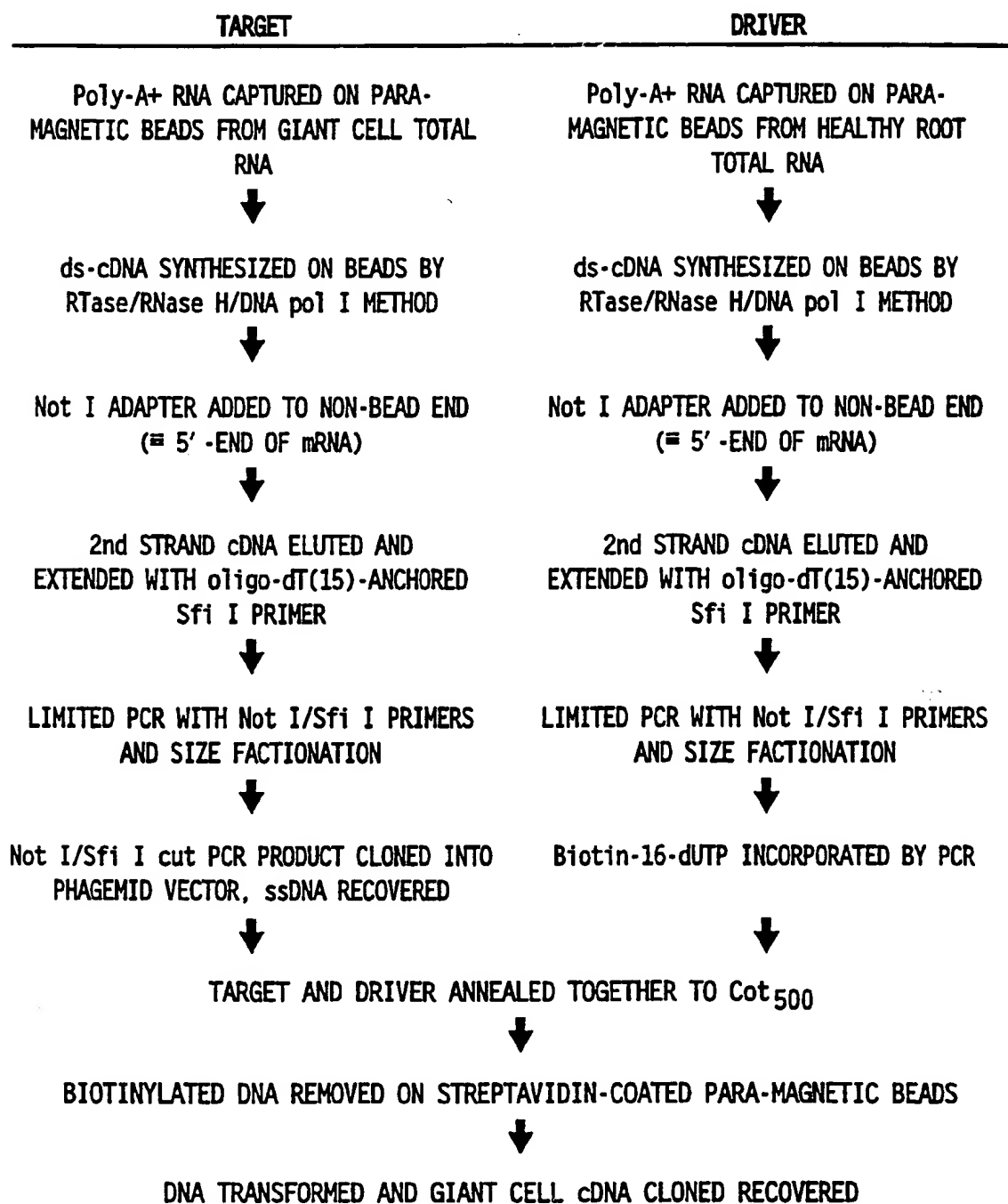
25
30

30. The method of claim 29, wherein the expression cassette is introduced into the plant using *Agrobacterium*.

31. The method of claim 29, wherein the plant is a tomato plant.

1/2

FIG. 1



2/2

FIG. 2

K PSSDS
 YK PSYDNS
 YKKPSYDSG
 YK PSYDNG
 YKKPSYDSG
 YK PSYDS
 YK PSYDN
 YK PSYDS
 YK PSYDN
 YK PSYDRL*

TS PSYSP

FIG. 3

DB#280:		QLOAKHGKWKIAAEVPGRTAKRLGKWEVSKRRQREQ
PETUNIA Ph3	[Z13998]	+L AK GNKW ++AA++PGRT + +W +R+QR
MOSS	[S24244]	L A GN+W +IAA++PGRT + +W +++ R Q
SNAPDRAGON 315	[JQ0961]	+L A GN+W KIA +PGRT + +W +++
BARLEY HV33	[P20027]	GN+W +IA+ +PGRT + +W +++ R+Q
SNAPDRAGON 308	[JQ0960]	+L + GNKW IA +PGRT + +W RR+
ARABIDOPSIS MYB1	[D10936]	A HGKWK IA +PGRT + W + RR+
MAIZE Zm.P1	[P27898]	+L A GN+W IA+ +PGRT + +W RQ
DROSOPHILA	[P04197]	Q + GN+W KIA +PGRT + W + RR+
HUMAN	[M13666]	Q + GN+W +IA +PGRT + W + RR+ ++

FIG. 4

TOBACCO: TGACCAGATAAAACAAATTTGTCTGATAAAGGGGGAAAACCTTTATCTTCTGTGATCTTCCCCCATC...

DB#226: ATAAACAAAAAACATGTCTTTAATATAAAGGGGGAAAACATTGTCTTGTGTGCTTTCCCCCTCTCA

TOBACCO: TATTTTACTTAACTTCGTTATGTATTTGATTTGAAGCGCCGCCATTGAAAGGGAGGGATTGTGTCCAA

DB#226: TCTATTCTTTAACTTCGTTATG...TTATATCTTGAAGCACCACCCATTGAA...AGGGATTGTGTCCAT

TOBACCO: GTTTTTTCCAACATTTTAATGGTGAAGTGACATCTCCTTGTAACAACACTACTACTCTTCCAAATTCACCTC

DB#226: GTTTTTTCCAAAATTTTAATGGTGAAGTGACATTTCTTGTAACAACAGT..TTTCTTACAATTTCTTCAC

TOBACCO: CTCTTTCTTTTTCTTGTGTTTTCAATTTGATGAGN₍₂₄₎-p1oyA

DB#226: CTCTTTTTTCTTCTT-polyA

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US95/06505

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 15/29, 15/82; A01H 4/00

US CL : 536/24.1, 23.2, 23.6; 435/320.1, 172.3; 800/205

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/24.1, 23.2, 23.6; 435/320.1, 172.3; 800/205, DIG 44

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN Biosis, SDC

Search terms: SEQ ID NO: 17, nematode(s), promoter(s), inducible, induced, responsive

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Science, Volume 263, issued 14 January 1994, C.H. Opperman et al., "Root-knot nematode-directed expression of a plant root-specific gene", pages 221-223, see the entire document.	1-31
Y	Journal of Cellular Biochemistry, Supplement 0 (18 Part A), issued 09-16 January 1994, O.J.M. Goddijn et al., "Analysis of gene activity in nematode-induced feeding structures, using promoter-GUS fusions and promoter tagging", page 93, abstract X1-133, see the entire abstract.	1-31

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

10 JULY 1995

Date of mailing of the international search report

05 SEP 1995

 Name and mailing address of the ISA/US
 Commissioner of Patents and Trademarks
 Box PCT
 Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

CHE SWYDEN CHERESKIN

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Nematology, Volume 25, Number 4, issued December 1993, C.L. Cramer et al., "Regulation of defense-related gene expression during plant-pathogen interactions", pages 507-518, see especially pages 513, column 2 to page 514.	1-31

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-31

Remark n Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/06505

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This ISA found multiple inventions as follows:

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

SEQ ID NOS: 1-109

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: SEQ ID NOS: 1-109 constitute a group of nucleic acid sequences which share neither the same structure nor function (see description, Table 1). Thus an objection of one sequence would be unlikely to be applicable for any other sequence in the group. Thus, each sequence is drawn to a different inventive concept. Accordingly, the claims are not so linked by a special technical feature within the meaning of PCT Rule 13.2 so as to form a single inventive concept. Applicants have elected the species SEQ ID NO: 17.